

GenCore version 5.1.6
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protein - protein search, using sw model

on: February 18, 2004, 06:03:18 ; Search time 44 Seconds
(without alignments)

41.537 Million cell updates/sec

le: US-09-806-376-1

fect score: 123

quence: 1 FNRCCCLIPACRRNHKKFC 19

ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

urched: 283366 seqs, 96191526 residues

al number of hits satisfying chosen parameters: 283366

imum DB seq length: 0

imum DB seq length: 2000000000

it-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

abase : PIR78:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query Match %	Length	DB ID	Description
1	52	42.3	189	T15479	hypothetical prote
2	50.5	41.1	720	T25883	hypothetical prote
3	49	39.8	67	T1ILP2	trypsin inhibitor
4	49	39.8	67	T1ILF3	trypsin inhibitor
5	49	39.8	640	T08179	LRG5 protein - Chl
6	48	39.0	16	A54877	alpha-conotoxin Pn
7	48	39.0	924	T09220	exocyst complex pr
8	47	38.2	257	A45753	folate-binding pro
9	46.5	37.8	48	S29973	protamine 1 - guin
10	46	37.4	57	S42778	relaxin - gorilla
11	46	37.4	174	T01649	probable trypsin i
12	46	37.4	185	A44559	relaxin 1 precursor
13	46	37.4	363	A48338	hypothetical prote
14	45.5	37.0	97	S59427	hypothetical prote
15	45	36.6	64	T1OAB	trypsin inhibitor
16	45	36.6	361	G70862	probable adheE2 pro
17	45	36.6	410	QRM8A1	thyroid hormone re
18	45	36.6	519	E64503	hypothetical prote
19	45	36.6	589	T36128	epithelin/granulin
20	45	36.6	593	1 GHYU	transposase Tam3 -
21	45	36.6	749	S13518	sperm histone 1 - sh
22	44.5	36.2	50	HS5H	sperm histone p1 -
23	44.5	36.2	51	HSBOS	aldehyde reductase
24	44.5	36.2	316	A60603	aldehyde reductase
25	44.5	36.2	316	T49484	multidrug resistan
26	44.5	36.2	1743	T24879	hypothetical prote
27	44.5	36.2	2561	T24864	alpha-conotoxin MI
28	44	35.8	16	A59046	alpha-conotoxin Ep
29	44	35.8	16	A59042	

ALIGNMENTS

RESULT 1

T15479
hypothetical protein C10A4.6 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 04-Mar-2000
C.Accession: T15479
R.Pauley, A.
submitted to the EMBL Data Library, March 1995
A.Description: The sequence of C. elegans cosmid C10A4.
A.Reference number: Z18358
A.Accession: T15479
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-189 <PAU>
A.Cross-references: EMBL:U23454; NID:G733580; PID:G733586; PIDN:AAC46520.1; CESP:C10A4
A.Experimental source: strain Bristol N2
C.Genetics:

A.Gene: CESP:C10A4.6
A.Introns: 40/1; 91/2; 119/1; 157/2
C.Superfamily: Caenorhabditis elegans hypothetical protein C10A4.6

Query Match 42.3%; Score 52; DB 2; Length 189;
Best Local Similarity 44.4%; Pred. No. 2.7;
Matches 12; Conservative 1; Mismatches 4; Indels 10; Gaps 1;

QY 1 FNRCCCLIPA-----CRNHKK 17

DB 144 FNRCCCYCATKMKLMNQICRRGKK 170

RESULT 2

T25883
hypothetical protein T10E9.2 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C.Accession: T25883
R.Greco, T.; Hawkins, M.
submitted to the EMBL Data Library, April 1997
A.Description: The sequence of C. elegans cosmid T10E9.
A.Reference number: Z20104
A.Accession: T25883
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-720 <GRE>
A.Cross-references: EMBL:U97403; PIDN:AAB52470.1; GSPDB:GN00019; CESP:T10E9.2
A.Experimental source: strain Bristol N2; clone T10E9
C.Genetics:

CAAX prenyl protei
aldose reductase h
hypothetical prote
aldehyde reductase
aldehyde reductase
hypothetical prote
folate-binding pro
hypothetical prote
folate-binding pro
probable alcohol d
cysteine proteinas
hypothetical prote
protein P52C13.4 [
hypothetical prote
aldehyde reductase
laminin-related pr
alpha-conotoxin Pn
hypothetical prote
SS RNA-binding pro
hypothetical prote
hypothetical prote

30 44 35.8 271 2 T37745

31 44 35.8 316 2 A53440

32 44 35.8 633 2 T23090

33 43.5 35.4 302 2 A34406

34 43.5 35.4 316 2 A59021

35 43.5 35.4 845 2 T13480

36 43 35.0 222 1 BFBO

37 43 35.0 249 2 S04674

38 43 35.0 255 2 A33417

39 43 35.0 361 2 A87132

40 43 35.0 416 2 G86232

41 43 35.0 678 2 G84682

42 43 35.0 1453 2 F88640

43 42.5 34.6 289 2 C96778

44 42.5 34.6 316 1 A39763

45 42.5 34.6 612 2 JH0799

46 42 34.1 16 2 B54877

47 42 34.1 274 2 T48296

48 42 34.1 365 2 C34895

49 42 34.1 426 2 T20265

50 42 34.1 702 2 T16832

Gene: CBSP.T10E9.2
 Gap position: 1
 Introns: 22/3; 52/1; 287/2; 340/3; 425/2; 476/2; 556/3; 697/2
 Superfamily: Caenorhabditis elegans hypothetical protein T10E9.2
 Query Match 41.1%; Score 50.5; DB 2; Length 720;
 Best Local Similarity 60.0%; Pred. No. 12;
 Matches 9; Conservative 0; Mismatches 3; Indels 3; Gaps 1;
 1 FNRCLIPACRNH 15
 |||||
 347 FXWRCL---CPAH 358
 |||||
 SULT 3
 ILF2
 Psin inhibitor (Bowman-Birk) II - foxtail millet
 Species: Setaria italica (foxtail millet)
 Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 31-Dec-1993
 Accession: JX0136
 Rashiro, M.; Asao, T.; Hirata, C.; Takahashi, K.; Kanamori, M.
 Biochem. 108, 669-672, 1990
 Title: The complete amino acid sequence of a major trypsin inhibitor from seeds of foxtail millet
 Reference number: JX0136; MUID:91154179; PMID:2292595
 Accession: JX0136
 Molecule type: protein
 Residues: 1-67 <TAS>
 Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
 Keywords: duplication; serine proteinase inhibitor
 9-34/Domain: Bowman-Birk inhibitor repeat homology <BB1>
 35-61/Domain: Bowman-Birk inhibitor repeat homology #status atypical <BB2>
 8-63,9-24,14-22,31-38,35-51/Disulfide bonds: #status predicted
 16/inhibitory site: Lys (trypsin) #status predicted
 Query Match 39.8%; Score 49; DB 1; Length 67;
 Best Local Similarity 35.3%; Pred. No. 3.4;
 Matches 6; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 3 WRCLIPACRNHKKFC 19
 |||||
 6 WKCCDLQCTKSIPAF 22
 |||||
 SULT 4
 ILF3
 Psin inhibitor (Bowman-Birk) III - foxtail millet
 Species: Setaria italica (foxtail millet)
 Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
 Accession: JG0013
 Rashiro, M.; Asao, T.; Hirata, C.; Takahashi, K.
 ric. Biol. Chem. 55, 419-426, 1991
 Title: Purification, characterization, and amino acid sequence of foxtail millet trypsin inhibitor
 Reference number: JG0013; MUID:91299279; PMID:1368693
 Accession: JG0013
 Molecule type: protein
 Residues: 1-67 <TAS>
 Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
 Keywords: duplication; serine proteinase inhibitor
 9-34/Domain: Bowman-Birk inhibitor repeat homology <BB1>
 35-61/Domain: Bowman-Birk inhibitor repeat homology #status atypical <BB2>
 8-63,9-24,14-22,31-38,35-51/Disulfide bonds: #status predicted
 16/inhibitory site: Lys (trypsin) #status predicted
 Query Match 39.8%; Score 49; DB 1; Length 67;
 Best Local Similarity 35.3%; Pred. No. 3.4;
 Matches 6; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 3 WRCLIPACRNHKKFC 19
 |||||
 6 WKCCDLQCTKSIPAF 22
 |||||

T08179
 LRGS protein - Chlamydomonas reinhardtii
 C:Species: Chlamydomonas reinhardtii
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
 C:Accession: T08179
 R;Gloeckner, G.; Beck, C.F.
 submitted to the EMBL Data Library, October 1996
 A:Description: Molecular characterization of a gene (LRGS) involved in blue light signal transduction
 A:Reference number: 216399
 A:Accession: T08179
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-640 <GLO>
 A:Cross-references: EMBL:U73817; NID:g1644369; PID:g1644370
 C:Genetics:
 A:Gene: LRGS
 Query Match 39.8%; Score 49; DB 2; Length 640;
 Best Local Similarity 60.0%; Pred. No. 18;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 NWRCLIPAC 11
 |||||
 DB 586 NWCCCLPGC 595
 |||||
 RESULT 6
 A:Accession: A54877
 A:Molecule type: protein
 A:Residues: 1-16 <FA>
 R;Hu, S.H.; Gehrmann, J.; Guddat, L.W.; Alewood, P.F.; Craik, D.J.; Martin, J.L.
 submitted to the Brookhaven Protein Data Bank, January 1996
 A:Reference number: A54877; PDB:1PEN
 A:Contents: annotation; X-ray crystallography, 1.1 angstroms; residues 1-16
 C:Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynaptic neurotoxin
 C:Superfamily: alpha-conotoxin
 C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neurotoxin
 F:2-8,3-16/Disulfide bonds: #status experimental
 F:16/Modified site: amidated carboxyl end (Cys) #status experimental
 Query Match 39.0%; Score 48; DB 2; Length 16;
 Best Local Similarity 40.0%; Pred. No. 1.6;
 Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 QY 5 CCLIPACRNHKKFC 19
 |||||
 DB 2 CCCLPPCAANNPDYC 16
 |||||
 RESULT 7
 T09220
 exocyst complex protein sec5 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
 C:Accession: T09220
 R;Kee, Y.; Yoo, J.S.; Hazuka, C.D.; Peterson, K.E.; Hsu, S.C.; Scheller, R.H.
 Proc. Natl. Acad. Sci. U.S.A. 94, 14438-14443, 1997
 A:Title: Subunit structure of the mammalian exocyst complex
 A:Reference number: 216617; MUID:98070770; PMID:9405631
 A:Accession: T09220
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-924 <KEE>

A; Experimental source: strain H37Rv
C; Genetix:
A; Gene: adhE2
C; Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
F; 352/Domain: long-chain alcohol dehydrogenase homology <ADH>

Query Match 36.6%; Score 45; DB 2; Length 361;
Best Local Similarity 40.0%; Pred. No. 43;
Matches 8; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

QY 2 NWR--CCLIPACRRNHKKFC 19
||| ||| : :
DB 88 NWRVCGGCRACKGRPRYC 107

RESULT 17
QRMSA1
thyroid hormone receptor alpha-1 - mouse
C; Species: Mus musculus (house mouse)
C; Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 22-Jun-1999
C; Accession: S14690; S08690
R; Masuda, M.; Yasuhara, S.; Yamashita, M.; Shibuya, M.; Odaka, T.
Nucleic Acids Res. 18, 3055, 1990
A; Title: Nucleotide sequence of the murine thyroid hormone receptor (alpha-1) cDNA.
A; Reference number: S14690; MUID:90272421; PMID:2349106
A; Accession: S14690
A; Status: translation not shown
A; Molecule type: mRNA
A; Residues: 1-410 <MAS>
A; Cross-references: EMBL:X51983; NID:G50385; PIDN:CAA36241.1; PID:G50386
C; Genetix:
A; Gene: erba-alpha
C; Superfamily: thyroid hormone receptor; erba transforming protein homology
C; Keywords: alternative splicing; DNA binding; proto-oncogene; thyroid hormone receptor
F; 51-327/Domain: erba transforming protein homology <ERBA>
F; 53-73/Region: zinc finger CCCC motif
F; 91-115/Region: zinc finger CCCC motif
F; 190-410/Domain: hormone binding #status predicted <HRB>

Query Match 36.6%; Score 45; DB 1; Length 410;
Best Local Similarity 46.7%; Pred. No. 47;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19
||| ||| : :
DB 96 CCVIDKTRNHQCQC 110

RESULT 18
E64503
hypothetical protein MJ1631 - Methanococcus jannaschii
C; Species: Methanococcus jannaschii
C; Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 22-Oct-1999
C; Accession: E64503
R; Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, A.;
Rosen, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A; Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A; Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A; Reference number: A64300; MUID:96337999; PMID:8688087
A; Accession: E64503
A; Status: Preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-519 <BUJ>
A; Cross-references: GB:U67603; GB:L77117; NID:G1592220; PIDN:AAB99652.1; PID:G1500530;
C; Genetix:
A; Map position: FOR1611185-1612744

Query Match 36.6%; Score 45; DB 2; Length 519;
Best Local Similarity 32.0%; Pred. No. 56;
Matches 8; Conservative 4; Mismatches 7; Indels 6; Gaps 1;


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MULT 21
[518
  inposase Tam3 - garden snapdragon transposon Tam3
  Species: Antirrhinum majus (garden snapdragon)
  Date: 18-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 21-Jul-2000
  Accession: S13518
  Author: Hehl, R.; Nacken, W.K.F.; Krause, A.; Siedler, H.; Sommer, H.
  Title: Structural analysis of Tam3, a transposable element from Antirrhinum majus, reveals a
  reference number: S13518; MUID:91370883; PMID:1654157
  Accession: S13518
  Status: preliminary
  Molecule type: DNA
  Residues: 1-749 <HEH>
  Cross-references: EMBL:X55078; NID:g16063; PIDN:CAA38906.1; PID:g16064
  Genbank:
  Mobile element: transposon Tam3
  Superfamily: hypothetical transposase Ac9
  Query Match 36.6%; Score 45; DB 2; Length 749;
  Best Local Similarity 44.4%; Pred. No. 73;
  Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
  2 NWRCCLIPACRRNHKKFC 19
  |||||
  142 NWAQCLLCPTRYSHKTCG 159
  |||||
MULT 22
[518
  arm histone - sheep
  Alternate names: cysteine-rich protamine; protamine
  Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
  Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 05-Sep-1997
  Accession: A02658
  Author: Gautiere, P.; Bellaiche, D.; Martinage, A.; Lohr, M.
  Title: Primary structure of the ram (Ovis aries) protamine.
  Reference number: A02658; MUID:85003651; PMID:6479168
  Accession: A02658
  Molecule type: protein
  Superfamily: sperm histone
  Keywords: chromosomal protein; DNA binding; nucleosome core; spermatogenesis
  F2-51/Product: protamine P1 #status experimental <MAR>
  F6/Disulfide bonds: interchain (to 22) #status predicted
  F7-15,40-48/Disulfide bonds: #status experimental
  F23/Disulfide bonds: interchain (to 5) #status predicted
  F39/Disulfide bonds: interchain #status predicted
  Query Match 36.2%; Score 44.5; DB 1; Length 50;
  Best Local Similarity 40.0%; Pred. No. 12;
  Matches 8; Conservative 4; Mismatches 5; Indels 3; Gaps 1;
  3 WRCCCLIPA---CRRNHKKFC 19
  :|||: :|||:
  3 YRCCLTHSGRCRRRRRC 22
  :|||: :|||:
MULT 23
[518
  arm histone P1 - bovine
  Alternate names: arginine-rich protamine; cysteine-rich protamine; protamine P1; sperm
  Species: Bos primigenius taurus (cattle)
  Date: 24-Apr-1984 #sequence_revision 30-Jun-1992 #text_change 22-Jun-1999
  Accession: A29911; A26450; A26041; A24375; A61342
  Author: Kravetz, S.A.; Connor, W.; Dixon, G.H.
  Title: Bovine protamine genes contain a single intron. The structures of the two alleles
  Reference number: A29911; MUID:88087109; PMID:3335501
  Accession: A29911
  Molecule type: DNA
  Residues: 1-51 <KTA>
  Cross-references: GB:M18396; NID:g163619; PIDN:AAA30735.1; PID:g163620

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R;Kravetz, S.A.; Connor, W.; Dixon, G.H.
DNA 6, 47-57, 1987
A>Title: Cloning of bovine P1 protamine cDNA and the evolution of vertebrate P1 protami
A;Reference number: A26450; MUID:87161234; PMID:3829889
A;Accession: A26450
A;Molecule type: mRNA
A;Residues: 1-51 <KR2>
A;Cross-references: GB:M14559; NID:g163632; PIDN:AAA30741.1; FID:g163633
R;Lee, C.H.; Mansouri, A.; Hecht, W.; Hecht, N.B.; Engel, W.
Biol. Chem. Hoppe-Seyler 368, 131-135, 1987
A>Title: Nucleotide sequence of a bovine protamine cDNA.
A;Reference number: A26041; MUID:87184911; PMID:2436637
A;Accession: A26041
A;Molecule type: mRNA
A;Residues: 2-51 <LER>
A;Cross-references: GB:M18625
A;Note: the codon for residue 30-Phe is shown as TCT
R;Mazrimas, J.A.; Corzett, M.; Campos, C.; Balhorn, R.
Biochim. Biophys. Acta 872, 11-15, 1986
A>Title: A corrected primary sequence for bull protamine.
A;Reference number: A24375; MUID:86269888; PMID:3730390
A;Accession: A24375
A;Molecule type: protein
A;Residues: 2-51 <MAZ>
R;Cooling, J.P.; Monfoort, C.H.; Rozijn, T.H.; Leuven, J.A.G.; Schiphof, R.; Steyn-Par
Biochim. Biophys. Acta 285, 1-14, 1972
A>Title: The complete amino acid sequence of the basic nuclear protein of bull spermato
A;Reference number: A61342; MUID:73124384; PMID:4675900
A;Accession: A61342
A;Molecule type: protein
A;Residues: 2-39;43-51 <COE>
R;Balhorn, R.; Corzett, M.; Mazrimas, J.; Watkins, B.
Biochemistry 10, 175-181, 1991
A>Title: Identification of bull protamine disulfides.
A;Reference number: A37137; MUID:91105078; PMID:1988019
A;Contents: annotation: disulfide bonds
C;Genetics:
A;Introns: 38/1
C;Function:
A;Description: binds to and packages sperm DNA in a condensed form of chromatin that is
C;Superfamily: sperm histone
C;Keywords: chromosomal protein; DNA binding; nucleosome core; spermatogenesis
F2-51/Product: protamine P1 #status experimental <MAR>
F6/Disulfide bonds: interchain (to 23) #status experimental
F7-15,40-48/Disulfide bonds: #status experimental
F23/Disulfide bonds: interchain (to 6) #status experimental
F39/Disulfide bonds: interchain #status experimental
Query Match 36.2%; Score 44.5; DB 1; Length 51;
Best Local Similarity 40.0%; Pred. No. 12;
Matches 8; Conservative 4; Mismatches 5; Indels 3; Gaps 1;
QY 3 WRCCCLIPA---CRRNHKKFC 19
:|||: :|||:
Db 4 YRCCLTHSGRCRRRRRC 23
:|||: :|||:
RESULT 24
A60603
N/Alternate names: aldose reductase
C/Species: Rattus norvegicus (Norway rat)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: A60603; S00079; B60603; I53649
R;Carper, D.A.; Wistow, G.; Nishimura, C.; Graham, C.; Watanabe, K.; Fujii, Y.; Hayashi
Exp. Eye Res. 49, 377-388, 1989
A>Title: A superfamily of NADPH-dependent reductases in eukaryotes and prokaryotes.
A;Reference number: A60603; MUID:90005742; PMID:2507340
A;Accession: A60603
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-316 <CAR>
R;Carper, D.; Nishimura, C.; Shinohara, T.; Dietzhold, B.; Wistow, G.; Craft, C.; Kado

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3S Lett. 220, 209-213, 1987
Title: Aldose reductase and rho-crystallin belong to the same protein superfamily as a
Reference number: S00079; MUID:87274556; PMID:3111886
Accession: S00079
Molecule type: mRNA
Residues: 33-316 <CA2>
Cross-references: EMBL:X05884
Note: 45-Ser and 54-Trp were also found
Accession: B60603
Molecule type: protein
Residues: 34-60, 'XX', 92-108, 146-173, 204-231, 244-252, 276-294 <CA3>
Note: Part of this sequence was confirmed by protein sequencing
Braham, C.E.; Szpirer, C.; Levan, G.; Carper, D.
Biochem. J. 107, 259-267, 1991
Title: Characterization of the aldose reductase-encoding gene family in rat.
Reference number: I53649; MUID:92084118; PMID:1748296
Accession: I53649
Status: translated from GB/EMBL/DBJ
Molecule type: DNA
Residues: 1-316 <RES>
Cross-references: GB:M60322; NID:G202851; PIDN:AAA40721.1; PID:G202852
Comment: Aldose reductase catalyzes reduction of a variety of sugars to sugar alcohols
Comment: This enzyme is active in the eye lens, where an accumulation of sugar alcohol
genetics:
Introns: 22/3; 78/3; 117/3; 143/3; 184/3; 220/2; 247/3; 275/3; 303/2
Superfamily: aldehyde reductase
Keywords: eye lens; NADP; oxidoreductase
263/Active site: Lys #status predicted
Query Match 36.2%; Score 44.5; DB 1; Length 316;
Best Local Similarity 41.2%; Pred. No. 46;
Matches 7; Conservative 4; Mismatches 5; Indels 1; Gaps 1;
2 NRCCCLIPACRRNHKPF 18
|||||:|:|:|:
295 NNRVCALMSCAK-HKDY 310
SULT 25
9484
aldehyde reductase (EC 1.1.1.21) - mouse
Species: Mus musculus (house mouse)
Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
Accession: I49484
Gui, T.; Tanimoto, T.; Kokai, Y.; Nishimura, C.
J. Biol. Chem. 227, 448-453, 1995
Title: Presence of a closely related subgroup in the aldo-ketoreductase family of the
Reference number: I49484; MUID:95154325; PMID:7851421
Accession: I49484
Status: preliminary; translated from GB/EMBL/DBJ
Molecule type: mRNA
Residues: 1-316 <RES>
Cross-references: GB:D32250; NID:G1384073; PIDN:BAA06980.1; PID:G786001
Superfamily: aldehyde reductase
Keywords: NADP; oxidoreductase
Query Match 36.2%; Score 44.5; DB 2; Length 316;
Best Local Similarity 41.2%; Pred. No. 46;
Matches 7; Conservative 4; Mismatches 5; Indels 1; Gaps 1;
2 NRCCCLIPACRRNHKPF 18
|||||:|:|:|:
295 NNRVCALMSCAK-HKDY 310
SULT 26
8279
ultradrug resistance transport protein - slime mold (Dictyostelium discoideum)
Species: Dictyostelium discoideum
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
Accession: T18279
Shaulsky, G.; Ucomis, W.F.
Submitted to the EMBL Data Library, June 1996

A;Reference number: Z18855
A;Accession: T18279
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1743 <SHA>
A;Cross-references: EMBL:U60086; NID:G1399914; PID:G1399915; PIDN:AAB03331.1
C;Genetics:
A;Gene: tagC
Query Match 36.2%; Score 44.5; DB 2; Length 1743;
Best Local Similarity 40.9%; Pred. No. 1.6e+02;
Matches 9; Conservative 2; Mismatches 6; Indels 5; Gaps 1;
QY 3 WRCCCLIPACRRNH-----KKFC 19
DB 933 WSSCLIQSCDNNYNSIKKRC 954
RESULT 27
T24864
hypothetical protein T12D8.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T24864; T27892
R;McMurray, A.
Submitted to the EMBL Data Library, October 1996
A;Reference number: Z19944
A;Accession: T24864
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-2561 <WIL>
A;Cross-references: EMBL:Z81120; PIDN:CAB03348.1; GSPDB:GN00021; CESP:T12D8.1
A;Experimental source: clone T12D8
R;Steward, C.
Submitted to the EMBL Data Library, November 1996
A;Reference number: Z20436
A;Accession: T27892
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-2561 <WI2>
A;Cross-references: EMBL:Z82094; PIDN:CAB05024.1; GSPDB:GN00021; CESP:T12D8.1
A;Experimental source: clone ZK525
C;Genetics:
A;Gene: CESP:T12D8.1
A;Map position: 3
A;Introns: 44/3; 78/3; 104/2; 251/2; 466/3; 504/3; 548/3; 662/2; 747/1; 962/1; 1355/3;
Query Match 36.2%; Score 44.5; DB 2; Length 2561;
Best Local Similarity 60.0%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
QY 3 WRCCCLIPACRR-NHK 16
DB 605 WRQWCSCRRCRNHK 619
RESULT 28
A59046
alpha-conotoxin MII - cone shell (Conus magus)
C;Species: Conus magus (magus cone)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: A59046
R;Cartier, G.E.; Yoshikami, D.; Gray, W.R.; Luo, S.; Olivera, B.M.; McIntosh, J.M.
J. Biol. Chem. 271, 7522-7528, 1996
A;Title: A new alpha-conotoxin which targets alpha3beta2 nicotinic acetylcholine receptor
A;Reference number: A59046; MUID:96205934; PMID:8631783
A;Accession: A59046
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <CAR>
C;Superfamily: alpha-conotoxin
C;Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro
F;1-16/Product: alpha-conotoxin MII #status experimental <MAI>

```

?-8,3-16/disulfide bonds: #status experimental
16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match      35.8%; Score 44; DB 2; Length 16;
Best Local Similarity 40.0%; Pred. No. 6.1;
Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

5 CCLIPACRNHHKFC 19
|||
2 CCNPNFVCHLSNLC 16

SULT 29
3042
pha-conotoxin Epi - cone shell (Conus episcopatus)
Species: Conus episcopatus (bishop's cone)
Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 13-Aug-1999
Accession: A59042
Joughnan, M.; Bond, T.; Atkins, A.; Cuevas, J.; Adams, D.J.; Broxton, N.M.; Livett, B.
Title: Alpha-conotoxin Epi, a novel sulfated peptide from Conus episcopatus that select
Reference number: A59042; MUID:98288307; PMID:9624161
Accession: A59042
Status: preliminary
Molecule type: protein
Residues: 1-16 <LOU>
Superfamily: alpha-conotoxin
Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; post-synaptic neuro
1-16/Product: alpha-conotoxin Epi #status experimental <MAT>
?-8,3-16/disulfide bonds: #status experimental
15/Binding site: sulfate (Tyr) (covalent) #status experimental
16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match      35.8%; Score 44; DB 2; Length 16;
Best Local Similarity 40.0%; Pred. No. 6.1;
Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

5 CCLIPACRNHHKFC 19
|||
2 CCSDPRCNWNPDC 16

SULT 30
7745
XX prenyl proteinase 2 - fission yeast (Schizosaccharomyces pombe)
Species: Schizosaccharomyces pombe
Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 07-Dec-1999
Accession: T37745
Medler, H.; Wambutt, R.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
Title: The prenyl proteinase 2 from Schizosaccharomyces pombe
Reference number: Z21744
Accession: T37745
Status: preliminary; translated from GB/EMBL/DBJ
Molecule type: DNA
Residues: 1-271 <WED>
Cross-references: EMBL:AL035064; PIDN:CAA2596.1; GSPDB:GN00066; SPDB:SPAC1687.02
Experimental source: strain 972h-; cosmid c1687
Genetics:
Gene: SPDB:SPAC1687.02
Map position: 1
Introns: 121/3

Query Match      35.8%; Score 44; DB 2; Length 271;
Best Local Similarity 55.6%; Pred. No. 48;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

3 WRCCLIIPAC 11
|||
130 FRCCIVPIC 138

SULT 31
3440
aldehyde reductase homolog - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 11-Jun-1999
C:Accession: A53440
R:Donohue, P.J.; Alberts, G.F.; Hampton, B.S.; Winkles, J.A.
J. Biol. Chem. 269, 8604-8609, 1994
A:Title: A delayed-early gene activated by fibroblast growth factor-1 encodes a protein
A:Reference number: A53440; MUID:94179253; PMID:7510692
A:Accession: A53440
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-316 <DON>
A:Cross-references: GB:U04204; NID:G463376; PIDN:AAA16953.1; PID:G463377
C:Superfamily: aldehyde reductase

Query Match      35.8%; Score 44; DB 2; Length 316;
Best Local Similarity 75.0%; Pred. No. 54;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 NWRCLIP 9
|||
DB      295 NWRACLLP 302

RESULT 32
T23030
hypothetical protein H13N06.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
A:Accession: T23030
R:Lennard, N.
submitted to the EMBL Data Library, October 1997
A:Reference number: Z19673
A:Accession: T23030
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-633 <WIL>
A:Cross-references: EMBL:Z99942; PIDN:CAB17071.1; GSPDB:GN00028; CESP:H13N06.6
C:Genetics:
C:Experimental source: clone H13N06
A:Gene: CESP:H13N06.6
A:Map position: X
A:Introns: 134/3; 179/3; 206/3; 381/2; 420/3; 541/2

Query Match      35.8%; Score 44; DB 2; Length 633;
Best Local Similarity 61.5%; Pred. No. 90;
Matches 8; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY      3 WRCLIPACRNH 15
|||
DB      50 WRCC--PRWRGNH 60

RESULT 33
A34406
aldehyde reductase (EC 1.1.1.21) - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 11-Jun-1999
C:Accession: A34406
R:Garcia-Perez, A.; Martin, B.; Murphy, H.R.; Uchida, S.; Murer, H.; Cowley Jr., B.D.;
J. Biol. Chem. 264, 16815-16821, 1989
A:Title: Molecular cloning of cDNA coding for kidney aldose reductase. Regulation of sp
A:Reference number: A34406; MUID:89380313; PMID:2506183
A:Accession: A34406
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-302 <GAR>
A:Cross-references: GB:J05048; NID:G164756; PIDN:AAA31157.1; PID:G164757
C:Superfamily: aldehyde reductase
C:Keywords: oxidoreductase

Query Match      35.4%; Score 43.5; DB 2; Length 302;
Best Local Similarity 41.2%; Pred. No. 62;

```

Matches 7; Conservative 4; Mismatches 5; Indels 1; Gaps 1;
 2 NWRCCCLIPACRRNHKKF 18
 |||||.:.:|:
 281 NWRVCALVSC-ASHKDY 296

SULT 34
 9021
 dehyde reductase (EC 1.1.1.21) [validated] - pig
 Species: Sus scrofa domestica (domestic pig)
 Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 15-Sep-2000
 Accession: A59021; A59019; S43018
 Kubiseki, T.J.; Green, N.C.; Flynn, T.G.
 v. Exp. Med. Biol. 328, 259-265, 1993
 Title: Location of an essential arginine residue in the primary structure of pig aldose
 Reference number: A59021; MUID:93263021; PMID:8493902
 Accession: A59021
 Molecule type: mRNA
 Residues: 1-316 <KUB>
 Cross-references: GB:U46065; NID:gl184819; PIDN:AAC48515.1; PID:gl184820
 Experimental source: adult brain
 Note: submitted to Genbank January 1996
 Jaquinod, M.; Potier, N.; Klarskov, K.; Reymann, J.M.; Sorokine, O.; Kieffer, S.; Bart
 r. J. Biochem. 218, 893-903, 1993
 Title: Sequence of pig lens aldose reductase and electrospray mass spectrometry of non
 Reference number: S43018; MUID:94109388; PMID:8281941
 Accession: A59019
 Molecule type: protein
 Residues: 2-98, 'D', 100-316 <JAQ1>
 Experimental source: eye lens
 Note: the authors found that a disulfide bond between residues 299-304 which they thou
 Accession: S43018
 Molecule type: protein
 Residues: 2-12 <JAQ2>
 Moras, D.; Podjarny, A.
 bmitted to the Brookhaven Protein Data Bank, April 1997
 Reference number: A69051; PDB:1AH4
 Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 2-98, 'D', 100-316
 Rondeau, J.M.; Tete-Favier, F.; Podjarny, A.; Reymann, J.M.; Barth, P.; Biellmann, J.H
 bmitted to the Brookhaven Protein Data Bank, February 1993
 Reference number: A52185; PDB:1DLA
 Contents: annotation; X-ray crystallography, 3.0 angstroms, residues 2-98, 'D', 100-316
 Genetics:
 Gene: ALR2
 Superfamily: aldehyde reductase
 Keywords: acetylated amino end; oxidoreductase
 2-316/Product: aldehyde reductase #status experimental <VAT>
 2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental

Query Match 35.4%; Score 43.5; DB 2; Length 316;
 Best Local Similarity 41.2%; Pred. NO. 64;
 Matches 7; Conservative 4; Mismatches 5; Indels 1; Gaps 1;
 2 NWRCCCLIPACRRNHKKF 18
 |||||.:.:|:
 295 NWRVCALMSC-ASHKDY 310

SULT 35
 3480
 trothetical protein 34F3.3 - fruit fly (Drosophila melanogaster)
 Species: Drosophila melanogaster
 Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jun-2000
 Accession: T13480
 Valentini, P.; Salles, C.; Campbell, L.; Glover, D.
 bmitted to the EMBL Data Library, April 1999
 Description: Sequencing the distal X chromosome of Drosophila melanogaster.
 Reference number: Z17685
 Accession: T13480
 Status: Preliminary; translated from GB/EMBL/DBJ
 Molecule type: DNA
 Residues: 1-845 <PHI>

A; Cross-references: EMBL:AL031583; NID:ei321005; PID:ei330107; PIDN:CAA20903.1
 C; Genetics:
 A; Gene: FlyBase:Rbf
 A; Cross-references: FlyBase:FBgn0015799
 A; Introns: 83/3; 110/2; 173/2; 291/3; 402/2; 647/3; 774/3
 Query Match 35.4%; Score 43.5; DB 2; Length 845;
 Best Local Similarity 61.5%; Pred. NO. 1.3e+02;
 Matches 8; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
 QY 2 NWRCCCLIPACRR 13
 |||||.:.:|:
 Db 68 HMMCCALYTACRR 80

Search completed: February 18, 2004, 06:04:20
 Job time : 46 secs

GenCore version 5.1.6
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protein - protein search, using sw model

on: February 18, 2004, 06:03:18 ; Search time 47 Seconds
(without alignments)
21.050 Million cell updates/sec

le: US-09-806-376-1

fect score: 123

quence: 1 FNWRCCLIPACRNHHKFC 19

ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 141681 seqs, 52070155 residues

al number of hits satisfying chosen parameters: 141681

imum DB seq length: 0

imum DB seq length: 2000000000

it-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

abase : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query Match	Length	ID	Description
1	123	100.0	19	1 CXR CONTU	P58811 conus tulip
2	49	39.8	67	1 IBB2 SEIT	P19860 setaria ita
3	49	39.8	67	1 IBB3 SEIT	P22737 setaria ita
4	48	39.0	16	1 CXAA CONTE	P50984 conus penna
5	48	39.0	66	1 CXA2 CONTE	Q9xzk7 conus texti
6	48	39.0	924	1 SEC5 MOUSE	Q9ddh1 mus musculus
7	48	39.0	924	1 SEC5 RAT	O54921 rattus norv
8	47	38.2	257	1 FOLL_HUMAN	P15328 homo sapien
9	46.5	37.8	47	1 HSP1_CAVPO	P35304 cavia porce
10	46	37.4	185	1 RELL_HUMAN	P04808 homo sapien
11	45.5	37.0	222	1 WED1_CHICK	Q8J933 gallus gall
12	45	36.6	64	1 IBB1 COILA	P07679 coix lachry
13	45	36.6	69	1 CXA1 CONTE	Q9xzk6 conus texti
14	45	36.6	519	1 YG31 METJA	Q59025 methanococc
15	45	36.6	593	1 GRN_HUMAN	P28799 h granulin
16	44.5	36.2	50	1 HSP1_BOVIN	P02318 bos taurus
17	44.5	36.2	50	1 HSP1_SHEEP	P04102 ovis aries
18	44.5	36.2	315	1 ALDR_MOUSE	P45376 mus musculus
19	44.5	36.2	315	1 ALDR RAT	P07943 rattus norv
20	44.5	36.2	1743	1 TAGC DICDI	Q23868 dictyosteli
21	44	35.8	16	1 CXA1 CONEP	P56638 conus epis
22	44	35.8	16	1 CXA2 CONNA	P56636 conus magus
23	44	35.8	271	1 RCEL_SCHPO	Q94448 schizosach
24	44	35.8	315	1 ALD2_MOUSE	P45377 mus musculus
25	44	35.8	360	1 FADH_AYME	P80094 amycolotops
26	44	35.8	924	1 SEC5_HUMAN	Q96kpl homo sapien
27	43.5	35.4	315	1 ALDR_PIG	P80276 sus scrofa
28	43.5	35.4	315	1 ALDR RABIT	P15122 coryctolagus
29	43.5	35.4	797	1 RBF_DROME	Q24472 drosophila
30	43.5	35.4	1218	1 JAG1_HUMAN	P78504 homo sapien
31	43	35.0	128	1 ACPS_EUCBP	P59475 bucinera ap
32	43	35.0	222	1 FOLL_BOVIN	P02702 bos taurus
33	43	35.0	249	1 YAT6_HOBL	P05449 rhodopsin

34	43	35.0	255	1 FOL2_HUMAN	P14207 homo sapien
35	43	35.0	678	1 MYH5_ARATH	Q9sl29 arabidopsis
36	43	35.0	1961	1 MYH9_RAT	Q62812 rattus norv
37	42.5	34.6	315	1 ALDR_HUMAN	P15121 homo sapien
38	42.5	34.6	612	1 UNC6_CABEL	P34710 caenorabdi
39	42.5	34.6	1218	1 JAG1_MOUSE	Q9gxx0 mus musculus
40	42	34.1	16	1 CXAB CONPE	P50985 conus penna
41	42	34.1	365	1 P43_XENLA	P25456 xenopus lae
42	42	34.1	452	1 KRMI_MOUSE	Q90y90 xenopus lae
43	42	34.1	473	1 KRMI_MOUSE	Q99n43 mus musculus
44	42	34.1	473	1 KRMI_RAT	Q92484 rattus norv
45	42	34.1	475	1 KRMI_HUMAN	Q96mu8 homo sapien
46	42	34.1	588	1 GRN_RAT	P23785 r granulin
47	42	34.1	607	1 ELM3_HUMAN	Q86yz7 mus musculus
48	42	34.1	671	1 ELM3_MOUSE	P16144 homo sapien
49	42	34.1	1822	1 ITB4_HUMAN	P49867 bombyx mori
50	41.5	33.7	555	1 FTF1_BOMMO	

ALIGNMENTS

RESULT 1

CXR CONTU STANDARD; PRT; 19 AA.

AC P58811: 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Rho-conotoxin T1A (Rho-T1A)

OS Conus tulipa (fish-hunting cone snail) (Tulip cone)

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;

OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hyposogastropoda;

OC Neogastropoda; Conoidea; Conidae; Conus.

OX NCBI_taxid=8495;

RN [1]

RP SEQUENCE, SYNTHESIS, AND STRUCTURE BY NMR.

RC TISSUE=Venom;

RX MEDLINE=21419681; PubMed=11528421;

RA Sharpe I.A., Gehrmann J., Loughnan M.L., Thomas L., Adams D.A.,

RA Atkins A., Palant E., Craik D.J., Adams D.J., Alewood P.F.,

RA Lewis R.J.;

RT "Two new classes of conopeptides inhibit the alpha-adrenoceptor and noradrenaline transporter.";

RL Nat. Neurosci. 4:902-907(2001).

CC -|- FUNCTION: Inhibits alpha-1 adrenergic receptors.

CC -|- SUBCELLULAR LOCATION: Secreted.

CC -|- TISSUE SPECIFICITY: Expressed by the venom duct.

CC -|- MASS SPECTROMETRY: MW=2390.15; METHOD=Electrospray.

CC -|- SIMILARITY: Belongs to the rho-conotoxin family.

DR PDB; 1IEN; 03-APR-02.

KW Toxin; Amidation; 3D-structure.

FT DISULFID 5 11

FT MOD_RES 6 19

FT TURN 12 3

FT TURN 19 19

FT TURN 2 3

FT HELIX 4 7

FT HELIX 9 12

FT TURN 13 14

FT TURN 14 14

FT HELIX 16 19

SQ SEQUENCE 19 AA; 2396 MW; C5917DDE62CA89DC CRC64;

Query Match 100.0%; Score 123; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.6e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNWRCCLIPACRNHHKFC 19

Db 1 FNWRCCLIPACRNHHKFC 19

RESULT 2

IBB2_SETIT

IBB2_SEQIT STANDARD; PRT; 67 AA.
 P19860;
 01-FEB-1991 (Rel. 17, Created)
 01-FEB-1991 (Rel. 17, Last sequence update)
 10-OCT-2003 (Rel. 42, Last annotation update)
 Bowman-Birk type major trypsin inhibitor (FMTI-II).
 Setaria italica (Foxtail millet).
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 PACCAD clade; Panicoideae; Paniceae; Setaria.
 NCBI_TaxID=4555;
 [1]
 SEQUENCE.
 MEDLINE=91154179; PubMed=2292595;
 Tashiro M., Asao T., Hirata C., Takahashi K., Kanamori M.;
 "The complete amino acid sequence of a major trypsin inhibitor from
 seeds of foxtail millet (Setaria italica).";
 J. Biochem. 108:669-672(1990).
 -!- SIMILARITY: Belongs to the Bowman-Birk serine protease inhibitor
 family.
 PIR; JX0136; TILF2.
 HSSP; P56679; 1PBI.
 InterPro; IPR000877; Bowman-Birk_leg.
 Pfam; PF00228; Bowman-Birk_leg; 2.
 ProDom; PD002168; Bowman-Birk_leg; 1.
 SMART; SM00269; BowB; 1.
 PROSITE; PS00281; BOWMAN_BIRK; 1.
 Serine protease inhibitor.
 ACT_SITE 16 17 INTERACTION WITH TRYPSIN (BY SIMILARITY).
 DISULFID 8 63 BY SIMILARITY.
 DISULFID 9 24 BY SIMILARITY.
 DISULFID 14 22 BY SIMILARITY.
 DISULFID 31 38 BY SIMILARITY.
 DISULFID 35 51 BY SIMILARITY.
 SEQUENCE 67 AA; 7679 MW; 109AF30F33248949 CRC64;
 Query Match 39.8%; Score 49; DB 1; Length 67;
 Best Local Similarity 35.3%; Pred. No. 0.73;
 Matches 6; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 3 WRCCCLIPACRRNHKFC 19
 6 WKCCDLQCTCKSIAPFC 22
 [1]
 SEQUENCE.
 MEDLINE=91299279; PubMed=1368693;
 Tashiro M., Asao T., Hirata C., Takahashi K.;
 "Purification, characterization, and amino acid sequence of foxtail
 millet trypsin inhibitor III.";
 Agric. Biol. Chem. 55:419-426(1991).
 -!- SIMILARITY: Belongs to the Bowman-Birk serine protease inhibitor
 family.
 PIR; JG0013; TILF3.
 HSSP; P56679; 1PBI.
 InterPro; IPR000877; Bowman-Birk_leg.
 Pfam; PF00228; Bowman-Birk_leg; 2.
 ProDom; PD002168; Bowman-Birk_leg; 1.
 SMART; SM00269; BowB; 1.

DR PROSITE; PS00281; BOWMAN_BIRK; 1.
 KW Serine protease inhibitor.
 FT ACT_SITE 16 17 INTERACTION WITH TRYPSIN (BY SIMILARITY).
 FT DISULFID 8 63 BY SIMILARITY.
 FT DISULFID 9 24 BY SIMILARITY.
 FT DISULFID 14 22 BY SIMILARITY.
 FT DISULFID 31 38 BY SIMILARITY.
 FT DISULFID 35 51 BY SIMILARITY.
 SQ SEQUENCE 67 AA; 7680 MW; 0D5AF30F33248949 CRC64;
 Query Match 39.8%; Score 49; DB 1; Length 67;
 Best Local Similarity 35.3%; Pred. No. 0.73;
 Matches 6; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 3 WRCCCLIPACRRNHKFC 19
 6 WKCCDLQCTCKSIAPFC 22
 [1]
 SEQUENCE.
 MEDLINE=94347719; PubMed=8068627;
 Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D.,
 Spira M.E., Zlotkin E.;
 "New mollusc-specific alpha-conotoxins block Aplysia neuronal
 acetylcholine receptors.";
 Biochemistry 33:9523-9529(1994).
 [2]
 Sulfation of TYR-15.
 MEDLINE=99242956; PubMed=10226369;
 Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M.,
 Baldwin M.A., Burlingame A.L.;
 "Identification of tyrosine sulfation in Conus pennaceus conotoxins
 alpha-PnIA and alpha-PnIB: further investigation of labile sulfo- and
 phosphopeptides by electrospray, matrix-assisted laser
 desorption/ionization (MALDI) and atmospheric pressure MALDI mass
 spectrometry.";
 J. Mass Spectrom. 34:447-454(1999).
 [3]
 X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
 MEDLINE=96311277; PubMed=8740364;
 Hu S.-H., Gehrmann J., Guddat L.W., Alewood P.F., Craik D.J.,
 Martin J.L.;
 "The 1.1 A crystal structure of the neuronal acetylcholine receptor
 antagonist, alpha-conotoxin PnIA from Conus pennaceus.";
 Structure 4:417-423(1996).
 -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
 bind to the nicotinic acetylcholine receptors (nAChR) and thus
 inhibit them. In contrast to other alpha-conotoxins, which are
 selective for vertebrate skeletal muscle nAChR, the Conus
 pennaceus alpha-conotoxins block nAChR in mollusks.
 -!- SUBCELLULAR LOCATION: Secreted.
 -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
 family.
 PIR; A54877; A54877.
 PDB; 1PEN; 21-APR-97.
 Postsynaptic neurotoxin; Neurotoxin; Toxin;
 Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.

RESULT 4


```

DISULFID 2 8
DISULFID 3 16
MOD_RES 15 15 SULFATION.
MOD_RES 16 16 AMIDATION.
HELIX 2 4
HELIX 6 11
TURN 13 16
SEQUENCE 16 AA; 1628 MW; 05310FF95EC99005 CRC64;
Query Match 39.0%; Score 48; DB 1; Length 16;
Best Local Similarity 40.0%; Pred. No. 0.26;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKFC 19
|||:|:|:|:|
2 CCSLPPCAANNPDYC 16

MULT 5
2_CONTE CONTE STANDARD; PRT; 66 AA.
Q9XZK7;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alpha-type conotoxin Tx2 precursor.
Conus textile (Cloth-of-gold cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=6494;
[1]
SEQUENCE FROM N.A.
TISSUE=Venom duct;
MEDLINE=20037955; PubMed=10573284;
Lu B.-S., Yu F., Zhao D., Huang P.-T., Huang C.-F.;
"Conopeptides from Conus striatus and Conus textile by cDNA
cloning.";
Peptides 20:1139-1144 (1999).
-!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
bind to the nicotinic acetylcholine receptors (nAChR) and thus
inhibit them (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom duct.
-!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
family.

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or send an email to license@isb-sib.ch).

EMBL; AF146353; AAD31913.1; -.
Postsynaptic neurotoxin; Neurotoxin; Toxin;
Acetylcholine receptor inhibitor; Signal.
SIGNAL 1 21 POTENTIAL.
PROPEP 22 49 BY SIMILARITY.
PEPTIDE 50 66 ALPHA-TYPE CONOTOXIN TX2.
DISULFID 51 57 BY SIMILARITY.
DISULFID 52 65 BY SIMILARITY.
SEQUENCE 66 AA; 7254 MW; EDD859BBA94F26F CRC64;
Query Match 39.0%; Score 48; DB 1; Length 66;
Best Local Similarity 46.7%; Pred. No. 1;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKFC 19
|||:|:|:|:|
51 CCSPACNVDPHC 65

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RESULT 6
SEC5_MOUSE
ID SEC5_MOUSE STANDARD; PRT; 924 AA.
AC Q9D4H1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Exocyst complex component Sec5.
GN SEC5 OR SEC5L1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=22354683; PubMed=12466851;
RA Okazaki I., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gasterland T., Gariboldi M., Gliss C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verrardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RA "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usslin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Beak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinaki M.I., Skalska U., Smalius D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
STRUCTURE BY NMR OF RALA-BINDING DOMAIN.

```

MEDLINE=22616004; PubMed=12624092;
Mott H.R., Nieflißpach D., Hopkins L.J., Mirey G., Camonis J.H.,
Owen D.,
"Structure of the GTPase-binding domain of Sec5 and elucidation of its
Ral binding site.",
J. Biol. Chem. 278:17053-17059(2003).
-!- FUNCTION: Component of the exocyst complex involved in the docking
of exocystic vesicles with fusions site on the plasma membrane (By
similarity).
-!- SUBUNIT: The exocyst complex is composed of SEC3, SEC5, SEC6,
SEC8, SEC10, SEC15, EXO70 and EXO84. Interacts with RALA and
GNFR/DELGF. Interaction with GNFR occurs only in the presence
of magnesium or manganese and is stimulated by dGTP or GTP.
-!- DOMAIN: Interacts with RALA through the TIG domain.
-!- SIMILARITY: Belongs to the SEC5 family.
-!- SIMILARITY: Contains 1 TIG domain.


```

NCBI_TaxID=10141;
[1]_SEQUENCE FROM N.A.
STRAIN=JML09;
Queralt R., Adroer R., Oliva R.;
Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: Protamines substitute for histones in the chromatin of
sperm during the haploid phase of spermatogenesis. They compact
sperm DNA into a highly condensed, stable and inactive complex.
-!- SUBUNIT: Cross-linked by interchain disulfide bonds around the
DNA-helix.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: Testis.
-!- SIMILARITY: Belongs to the protamine P1 family.
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EMBL; M83896; AAA58349.1; -
EMBL; Z11544; CAA77643.1; -
EMBL; Z11545; CAA77644.1; -
PIR; S29973; S29973.
InterPro; IPR000221; Protamine P1.
Pfam; PF00260; protamine P1; 1.
PROSITE; PS00048; PROTAmine P1; 1.
Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
Testis; DNA condensation; Nuclear protein.
INIT MET 0 BY SIMILARITY.
SEQUENCE 47 AA; 6553 MW; D93710VE37DE704D CRC64;
Query Match 37.8%; Score 46.5; DB 1; Length 47;
Best Local Similarity 42.1%; Pred. No. 1.2;
Matches 8; Conservative 4; Mismatches 4; Indels 3; Gaps 1;
3 WRCCLIPA---CRNKKYF 18
:|||||:|||||:|
3 YRCRSPGRRCRRRRRP 21
[1]
HUMAN STANDARD; PRT; 185 AA.
P04808; Q99936; Q9UQJ1;
13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Prorelaxin H1 precursor.
RLN1.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=85051298; PubMed=6548702;
Hudson P., John M., Crawford R., Haralambidis J., Scanlon D.,
Gorman J., Tregear G., Shine J., Niall H.;
"Relaxin gene expression in human ovaries and the predicted structure
of a human preprorelaxin by analysis of cDNA clones."
EMBO J. 3:2333-2339(1984).
[2]
SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=83141755; PubMed=6298628;
Hudson P., Haley J., John M., Cronk M., Crawford R., Haralambidis J.,
Tregear G., Shine J., Niall H.;
"Structure of a genomic clone encoding biologically active human
relaxin."
Nature 301:628-631(1983).

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RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Serra H.; (AUG-2000) to the EMBL/GenBank/DBJ databases.
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield V.S.N., Kzywinski M.I., Skalska U., Smalus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP PARTIAL SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE
SPECIFICITY.
RC TISSUE=Prostate;
RX MEDLINE=96328899; PubMed=8735594;
RA Gundersen J.M., Fu P., Roche P.J., Tregear G.W.;
"Expression of human relaxin genes: characterization of a novel
alternatively-spliced human relaxin mRNA species."
Mol. Cell. Endocrinol. 118:85-94(1996).
RN [6]
RP SEQUENCE OF 1-11 FROM N.A.
RA Garibay-Tupas J.;
RT "Characterization of the human H1 relaxin 5'-flanking region."
Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RL -!- FUNCTION: Relaxin is an ovarian hormone that acts with estrogen to
produce dilatation of the birth canal in many mammals. May be
involved in remodeling of connective tissues during pregnancy,
promoting growth of pubic ligaments and ripening of the cervix.
-!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
disulfide bonds.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=PC4808-1; Sequence=Displayed;
CC Name=2;
CC IsoId=PC4808-2; Sequence=VSP_002709; VSP_002710;
CC -!- TISSUE SPECIFICITY: Prostate. Not expressed in placenta, decidua
or ovary.
CC -!- SIMILARITY: Belongs to the insulin family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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EMBL; X00949; CAA25461.1; -
EMBL; V00578; CAA23839.1; -
EMBL; V00577; CAA23838.1; -
EMBL; AF104934; AAD21967.1; -
EMBL; A06926; CAA00603.1; -

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EMBL; A06846; CAA00599.1; -
EMBL; A07364; CAA00658.1; -
EMBL; A17329; CAA01325.1; -
EMBL; A1135786; CAC04179.1; -
EMBL; BC005956; AA005956.1; -
EMBL; S83200; AAD14429.1; -
PIR; B05092; A44559.
HSP; P04090; 6RLX.
Genew; HGNC:10026; RLN1.
MIM; 179730; -
GO; GO:0005180; F:peptide hormone; TAS.
InterPro; IPR004825; Ins/IGF/relax.
Pfam; PF00049; Insulin; 1.
SMART; SM00078; IIGF; 1.
PROSITE; PS00262; INSULIN; 1.
Insulin family; Hormone; Multigene family; Signal;
Alternative splicing; Polymorphism.
SIGNAL 1 22 PROBABLE.
CHAIN 23 53 RELAXIN B CHAIN (PROBABLE).
PROPEP 56 158 CONNECTING PEPTIDE (PROBABLE).
CHAIN 163 185 RELAXIN A CHAIN (PROBABLE).
DISULFID 35 172 INTERCHAIN (BY SIMILARITY).
DISULFID 47 185 INTERCHAIN (BY SIMILARITY).
DISULFID 171 176 BY SIMILARITY.
VARSPLIC 71 117 RIVPSFKDPTETIIIMLERIANLPKLKAALSEROPSLE
LOOKVP -> GDFIQTVSLGISPDGKKALETGSCFTREFLG
ALSKLYHPSSTKIOKL (in isoform 2).
/FTID=VSP_002709.
Missing (in isoform 2).
/FTID=VSP_002710.
K -> M (in dbSNP:618066).
/FTID=VAR_011962.
SEQUENCE 185 AA; 21145 MW; B318628ABFE7142 CRC64;

Query Match 37.4%; Score 46; DB 1; Length 185;
Best Local Similarity 43.8%; Pred. No. 5.3;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

4 RCCLIPACRRNHKKFC 19
|||||
170 KCCLIGTKRSIAKVC 185

MULT 11
11 CHICK
WFD1 CHICK STANDARD; PRT; 222 AA.
O8JC3.
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
WAP four-disulfide core domain protein 1 precursor (ps20 protein).
WFD1 OR PS20.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Gallus.
NCBI_TaxID=9031;
[1]
SEQUENCE FROM N.A.
Lopez-Viado C., Galetto R., Piedra E., Ros M., Rodriguez-Rey J.C.;
"cps20 is differentially expressed in chicken limb buds.";
Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: Has growth inhibitory activity (By similarity).
-!- SUBCELLULAR LOCATION: Secreted (potential).
-!- SIMILARITY: Contains 1 WAP-type domain.

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EMBL; AJ438290; CAD27352.1; -
InterPro; IPR008197; WAP.
Pfam; PF00095; wap; 1.
SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
KW Serine protease inhibitor; signal.
FT SIGNAL 1 32 POTENTIAL.
FT CHAIN 33 222 WAP FOUR-DISULFIDE CORE DOMAIN PROTEIN 1.
FT DOMAIN 64 109 WAP.
FT DOMAIN 69 72 POLY-PRO.
FT DISULFID 68 98 BY SIMILARITY.
FT DISULFID 80 102 BY SIMILARITY.
FT DISULFID 85 97 BY SIMILARITY.
FT DISULFID 91 106 BY SIMILARITY.
SQ SEQUENCE 222 AA; 25235 MW; CD8B00BD1CED5BEB CRC64;

Query Match 37.0%; Score 45.5; DB 1; Length 222;
Best Local Similarity 36.1%; Pred. No. 7.5;
Matches 8; Conservative 3; Mismatches 5; Indels 5; Gaps 1;

QY 4 RCCLIPACR-----RNHKKFC 19
| | | | |
DB 78 RACEVPSCRSDSECRHKCC 98

RESULT 12
ID IBBI COILA STANDARD; PRT; 64 AA.
AC P07679;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Bowman-Birk type trypsin inhibitor T11.
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Coix.
OX NCBI_TaxID=4505;
RN [1]
RP
RP MEDLINE=89152203; PubMed=3162215;
RX ARY M.B., Shewry P.R., Richardson M.;
RT "The amino acid sequence of a cereal Bowman-Birk type trypsin
inhibitor from seeds of Jobs' tears (Coix lachryma-jobi L.)";
RL FEBS Lett. 229:111-118(1988).
CC -!- SIMILARITY: Belongs to the Bowman-Birk serine protease inhibitor
family.
CC PIR; S00349; TIOAB.
CC HSP; P56679; IPBI.
DR InterPro; IPR00877; Bowman-Birk_leg.
DR Pfam; PF00228; Bowman-Birk_leg; 2.
DR ProDom; PD002168; Bowman-Birk_leg; 1.
DR SMART; SM00269; BOWB; 1.
DR PROSITE; PS00281; BOWMAN_BIRK; 1.
KW Serine protease inhibitor.
FT ACT SITE 17 18 INTERACTION WITH TRYPSIN (BY SIMILARITY).
FT DISULFID 9 61 BY SIMILARITY.
FT DISULFID 10 25 BY SIMILARITY.
FT DISULFID 15 23 BY SIMILARITY.
FT DISULFID 32 39 BY SIMILARITY.
FT DISULFID 36 49 BY SIMILARITY.
SQ SEQUENCE 64 AA; 7270 MW; 2ED0EEFF063E891 CRC64;

Query Match 36.6%; Score 45; DB 1; Length 64;
Best Local Similarity 41.2%; Pred. No. 2.7;
Matches 7; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 WRCLIPACRRNHKKFC 19
| | | | |
DB 7 WECDDIAMCTRSIPIC 23

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SULT 13

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11- CONTE STANDARD; PRT; 69 AA.
Q9XZK6;
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alpha-type conotoxin Tx1 precursor.
Conus textile (Cloth-of-gold cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbecconcha; Hypogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=6494;
[1]
SEQUENCE FROM N.A.
TISSUE=Venom duct;
MEDLINE=20037955; PubMed=10573284;
Lu B.-S., Yu F., Zhao D., Huang P.-T., Huang C.-F.;
"Conopeptides from Conus striatus and Conus textile by cDNA
cloning.";
Peptides 20:1139-1144(1999).
-!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
bind to the nicotinic acetylcholine receptors (nAChR) and thus
inhibit them (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom duct.
-!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
family.
-----
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EMBL; AF146352; AAD31912.1;
Postsynaptic neurotoxin; Neurotoxin; Toxin;
Acetylcholine receptor inhibitor; Signal; Amidation.
SIGNAL 1 21
POTENTIAL.
PROPEP 22 49 BY SIMILARITY.
PEPTIDE 50 66 ALPHA-TYPE CONOTOXIN TX1.
DISULFID 51 57 BY SIMILARITY.
DISULFID 52 65 BY SIMILARITY.
MOD RES 66 66 AMIDATION (G-67 PROVIDE AMIDE GROUP).
SEQUENCE 69 AA; 7442 MW; E36ECE90BF1B56B0 CRC64;
Query Match 36.6%; Score 45; DB 1; Length 69;
Best Local Similarity 40.0%; Pred. No. 2.9;
Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
5 CCLIPACRRNKKFC 19
51 CCSDPRCNSHPCLC 65
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SULT 14
31- METJA STANDARD; PRT; 519 AA.
Q59025;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein MJ1631.
Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
NCBI_TaxID=2190;
[1]
SEQUENCE FROM N.A.
STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

```

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RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klank H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii.";
Science 273:1058-1073(1996).
RL Science 273:1058-1073(1996).
CC -!- SIMILARITY: Belongs to the glycogen phosphorylase family.
CC
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or send an email to license@isb-sib.ch).
-----
EMBL; U67603; AAB99652.1;
DR PIR; E64503; E64503.
DR TIGR; MJ1631.
DR InterPro; IPR000811; Glyco trans 35.
DR PROSITE; PS0102; PHOSPHORYLASE; FALSE_NEG.
DR Hypothetical protein; Complete proteome.
KW SEQUENCE 519 AA; 60469 MW; D2C9D64C7C0D2093 CRC64;
Query Match 36.6%; Score 45; DB 1; Length 519;
Best Local Similarity 32.0%; Pred. No. 20;
Matches 8; Conservative 4; Mismatches 7; Indels 6; Gaps 1;
QY 1 FNRCCUIPACRR-----NHKKFC 19
DB 231 FNTVTCALRVCKRANAVSKKKEVC 255
-----
RESULT 15
GRN_HUMAN STANDARD; PRT; 593 AA.
ID GRN_HUMAN PRT; 593 AA.
AC P28799; P23781; P23782; P23783; P23784; Q95WE7;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Granulin precursor (Acrogranin) (Proepithelin) (PEPI) [Contains:
DE Granulin; Granulin 1 (Granulin G); Granulin 2 (Granulin F);
DE Granulin 3 (Granulin B); Granulin 4 (Granulin A); Granulin 5 (Granulin
DE C); Granulin 6 (Granulin D); Granulin 7 (Granulin E)].
GN GRN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Bone marrow;
RX MEDLINE=92179253; PubMed=1542665;
RA Bhandari V., Palfrey R.G.E., Bateman A.;
RT "Isolation and sequence of the granulin precursor cDNA from human
RT bone marrow reveals tandem cysteine-rich granulin domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:1715-1719(1992).
RN [2]
RP REVISIONS, SEQUENCE FROM N.A.
RX MEDLINE=93038704; PubMed=1417868;
RA Bhandari V., Bateman A.;
RT "Structure and chromosomal location of the human granulin gene.";
RL Biochem. Biophys. Res. Commun. 188:57-63(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=92317004; PubMed=1618805;

```

Plowman G.D., Green I.M., Neubauer M.G., Buckley S.D., McDonald V.L.,
 Todaro G.J., Shoyab M.;
 "The epithelin precursor encodes two proteins with opposing activities
 on epithelial cell growth";
 J. Biol. Chem. 267:13073-13078 (1992).

[4]
 SEQUENCE FROM N.A.
 TISSUE=Brain;
 Yu W., Gibbs R.A.;

Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 [5]
 SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 TISSUE=Cervix, and Lung;

MEDLINE=22389257; PubMed=12477932;
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettman M., Maman A., Rodriguez S., Sanchez A.,
 Whiting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).

[6]
 SEQUENCE OF 206-233; 281-336; 364-396 AND 442-447.
 TISSUE=Leukocyte;

MEDLINE=91097544; PubMed=22683320;
 Bateman A., Belcourt D.R., Bennett H.P., Lazure C., Solomon S.;
 "Granulins, a novel class of peptide from leukocytes";
 Biochem. Biophys. Res. Commun. 173:1161-1168(1990).
 -!- FUNCTION: Granulins have possible cytokine-like activity. They may
 play a role in inflammation, wound repair, and tissue remodeling.
 -!- FUNCTION: Granulin A promotes proliferation of the epithelial cell
 line A431 in culture while granulin B acts as an antagonist to
 granulin A, inhibiting the growth.
 -!- SUBCELLULAR LOCATION: Secreted.
 -!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;
 Name=1;
 IsoId=P28799-1; Sequence=Displayed;
 Name=2;
 IsoId=P28799-2; Sequence=VSP_001837;
 Note=No experimental confirmation available;
 -!- TISSUE SPECIFICITY: In myelogenous leukemic cell lines of
 promonocytic, promyelocytic, and proerythroid lineage, in
 fibroblasts, and very strongly in epithelial cell lines. Present
 in inflammatory cells and bone marrow. Highest levels in kidney.
 -!- PTM: Granulins are disulfide bridged.
 -!- SIMILARITY: Belongs to the granulin family.

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 or send an email to license@isb-sib.ch).

EMBL; M75161; AA58617.1; ALT_SEQ.
 EMBL; X62320; CA444196.1; --
 EMBL; AF055008; AAC09359.1; --
 EMBL; BC000324; AAH00324.1; --

DR EMBL; BC010577; AAH10577.1; --
 DR PIR; JCI284; GYHU.
 DR PDB; 1G36; 01-NOV-00.
 DR Genew; HGNC:4601; GRN.
 DR MIM; 138945; --
 DR GO; GO:0008083; F: growth factor activity; TAS.
 DR InterPro; IPR000118; Granulin.
 DR Pfam; PF00396; granulin; 7.
 DR SMART; SM00277; GRAN; 7.
 DR PROSITE; PS00799; GRANULINS; 7.
 KW Cytokine; Repeat; Glycoprotein; Signal; Alternative splicing;
 KW Polymorphism; 3D-structure.
 FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 18 593 ACROGRANIN.
 FT PEPTIDE 18 747 PARAGRANULIN.
 FT PEPTIDE 758 7113 GRANULIN 1.
 FT PEPTIDE 7123 7179 GRANULIN 2.
 FT PEPTIDE 205 261 GRANULIN 3.
 FT PEPTIDE 281 336 GRANULIN 4.
 FT PEPTIDE 364 7417 GRANULIN 5.
 FT PEPTIDE 442 7496 GRANULIN 6.
 FT PEPTIDE 7518 7573 GRANULIN 7.
 FT CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 236 236 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 368 368 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 530 530 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 377 531 Missing (in isoform 2).
 FT VARIANT 454 454 /FTIG=VSP_001837.
 FT VARIANT 454 454 G -> Q.
 FT VARIANT 515 515 /FTIG=VAR_003445.
 FT VARIANT 515 515 G -> A (in dbSNP:25647).
 FT CONFLICT 219 219 S -> H (in REF. 6).
 FT CONFLICT 386 386 W -> H (in REF. 6).
 SQ SEQUENCE 593 AA; 63473 MW; 4E402BDB16DE2819 CRC64;
 Query Match 36.6%; Score 45; DB 1; Length 593;
 Best Local Similarity 42.1%; Pred. No. 23;
 Matches 8; Conservative 2; Mismatches 7; Indels 2; Gaps 1;
 Qy 3 WRCLIP--ACRRNHKKFC 19
 Db 386 WGCCPIPEAVCCSDHQHC 404
 RESULT 16
 HSPI_BOVIN
 ID HSPI_BOVIN STANDARD; PRT; 50 AA.
 AC P02318;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Sperm protamine P1 (Cysteine-rich protamine).
 GN PRM1 OR PRM-1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=87161234; PubMed=3829989;
 RA Krawetz S.A., Connor W., Dixon G.H.;
 RT "Cloning of bovine P1 protamine cDNA and the evolution of vertebrate
 P1 protamines";
 RL DNA 6:47-57(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=88087109; PubMed=3335501;
 RA Krawetz S.A., Connor W., Dixon G.H.;
 RT "Bovine protamine genes contain a single intron. The structures of
 the two alleles";

J. Biol. Chem. 263:321-326 (1988).

[3] SEQUENCE FROM N.A.
MEDLINE=87184911; PubMed=2436637;
Lee C.-H., Mansouri A., Hecht W., Hecht N.B., Engel W.;
"Nucleotide sequence of a bovine protamine cDNA.";
Biol. Chem. Hoppe-Seyler 368:131-135 (1987).

[4] SEQUENCE.
MEDLINE=86269988; PubMed=37030390;
Mazzimas J.A., Corzett M., Campos C., Balhorn R.;
"A corrected primary sequence for bull protamine.";
Biochim. Biophys. Acta 872:11-15 (1986).

[5] SEQUENCE.
MEDLINE=73124384; PubMed=4675900;
Coelingh J.P., Monfoort C.H., Rozijn T.H., Gevers Leuven J.A.,
Schiphof R., Steyn-Parve E.P., Braunitzer G., Schrank B., Ruitus A.;
"The complete amino acid sequence of the basic nuclear protein of
bull spermatozoa.";
Biochim. Biophys. Acta 285:1-14 (1972).

[6] DISULFIDE BONDS.
MEDLINE=91105078; PubMed=1988019;
Balhorn R., Corzett M., Mazzimas J., Watkins B.;
"Identification of bull protamine disulfides.";
Biochemistry 30:175-181 (1991).

-!- FUNCTION: Protamines substitute for histones in the chromatin of
sperm during the haploid phase of spermatogenesis. They compact
sperm DNA into a highly condensed, stable and inactive complex.

-!- SUBUNIT: Cross-linked by interchain disulfide bonds around the
DNA-helix.

-!- SUBCELLULAR LOCATION: Nuclear.

-!- TISSUE SPECIFICITY: Testis.

-!- SIMILARITY: Belongs to the protamine P1 family.

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EMBL; M14559; AAA30741.1; -
EMBL; M18396; AAA30735.1; -
EMBL; M18395; AAA30736.1; -
EMBL; M18625; AAA30742.1; -
PIR; A23911; HSB08.
InterPro: IPR000221; Protamine_P1.
Pfam: PF00260; protamine P1; 1.
PROSITE; PS00048; PROTAMINE_P1; 1.
Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
Testis; DNA condensation; Nuclear protein.

INIT MET 0 0 INTERCHAIN (WITH C-22).
DISULFID 5 5
DISULFID 6 14
DISULFID 22 22 INTERCHAIN (WITH C-5).
DISULFID 38 38 INTERCHAIN (WITH C-38).
DISULFID 39 47
CONFLICT 29 29 F -> S (IN REF. 3).
CONFLICT 39 41 MISSING (IN REF. 5).
SEQUENCE 50 AA; 6627 MW; 932A69D98D30D2C7 CRC64;

Query Match 36.2%; Score 44.5; DB 1; Length 50;
Best Local Similarity 40.0%; Pred. No. 2.6;
Matches 8; Conservative 4; Mismatches 5; Indels 3; Gaps 1;
Matches 8; Conservative 4; Mismatches 5; Indels 3; Gaps 1;

3 WRCCCLIPA---CRNHKKFC 19
:||||:||||:
3 YRCCLTHSGRCRRRRRC 22

RESULT 17
HSP1 SHEEP STANDARD; PRT; 50 AA.
AC P04102;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sperm protamine P1 (Cysteine-rich protamine).
GN PRM1 OR PRM-1.
OS Ovis aries (Sheep), and
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940, 9925;
RN [1]
RP SEQUENCE.
RC SPECIES=Sheep;
RX MEDLINE=85003651; PubMed=6479168;
RA Sautiere P., Belaiche D., Martinage A., Loir M.;
RT "Primary structure of the ram (Ovis aries) protamine.";
RL Eur. J. Biochem. 144:121-125 (1984).
RN [2]
RP SEQUENCE.
RC SPECIES=C.hircus;
RX MEDLINE=89078594; PubMed=3060372;
RA Ammer H., Henschen A.;
RT "Primary structure of rabbit sperm protamine, the first protamine of
its type with an aberrant N-terminal.";
RL FEBS Lett. 242:111-115 (1988).
CC -!- FUNCTION: Protamines substitute for histones in the chromatin of
sperm during the haploid phase of spermatogenesis. They compact
sperm DNA into a highly condensed, stable and inactive complex.

CC -!- SUBUNIT: Cross-linked by interchain disulfide bonds around the
DNA-helix (By similarity).

CC -!- SUBCELLULAR LOCATION: Nuclear.

CC -!- TISSUE SPECIFICITY: Testis.

CC -!- SIMILARITY: Belongs to the protamine P1 family.

DR PIR; A02658; HSSH.
DR InterPro; IPR000221; Protamine_P1.
DR Pfam; PF00260; protamine P1; 1.
DR PROSITE; PS00048; PROTAMINE_P1; 1.
KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
KW Testis; DNA condensation; Nuclear protein.

FT DISULFID 5 5 INTERCHAIN (WITH C-22) (BY SIMILARITY).
FT DISULFID 6 14 BY SIMILARITY.
FT DISULFID 22 22 INTERCHAIN (WITH C-5) (BY SIMILARITY).
FT DISULFID 38 38 INTERCHAIN (WITH C-38) (BY SIMILARITY).
FT DISULFID 39 47 BY SIMILARITY.
SQ SEQUENCE 50 AA; 6712 MW; 6B2A78D98D2242DA CRC64;

Query Match 36.2%; Score 44.5; DB 1; Length 50;
Best Local Similarity 40.0%; Pred. No. 2.6;
Matches 8; Conservative 4; Mismatches 5; Indels 3; Gaps 1;
Matches 8; Conservative 4; Mismatches 5; Indels 3; Gaps 1;

QY 3 WRCCCLIPA---CRNHKKFC 19
:||||:||||:
Db 3 YRCCLTHSGRCRRRRRC 22

RESULT 18
ALDR MOUSE STANDARD; PRT; 315 AA.
AC P45376; Q70130; Q99KC9;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Aldose reductase (EC 1.1.1.21) (AR) (Aldehyde reductase).
GN AKR1B1 OR ALDR1 OR ALDR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;

[1] SEQUENCE FROM N.A.
 STRAIN=C57BL/6; TISSUE=Kidney;
 MEDLINE=95154325; PubMed=7851421;
 "Presence of a closely related subgroup in the aldo-ketoreductase family of the mouse."
 Eur. J. Biochem. 227:448-453 (1995).

[2] SEQUENCE FROM N.A.
 STRAIN=ICR X Swiss Webster; TISSUE=Liver;
 Iwata T., Carper B.;
 Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.

[3] SEQUENCE FROM N.A.
 STRAIN=CD-1; TISSUE=Kidney;
 Daoudal S., Berger M., Pailhoux E., Tournaire C., Veyssiere G.,
 Jean C.;
 Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.

[4] SEQUENCE FROM N.A.
 STRAIN=129/Ola;
 MEDLINE=98153248; PubMed=9485495;
 McGowan M.H., Iwata T., Carper D.A.;
 "Characterization of the mouse aldoase reductase gene and promoter in a lens epithelial cell line."
 Mol. Vision 4:2-2 (1998).

[5] SEQUENCE FROM N.A.
 STRAIN=129/SVJ;
 MEDLINE=99192817; PubMed=10092857;
 Ho H.T.B., Jenkins N.A., Copeland N.G., Gilbert D.J., Winkles J.A.,
 Louie H.W.Y., Lee F.K., Chung S.S.M., Chung S.K.;
 "Comparisons of genomic structures and chromosomal locations of the mouse aldoase reductase and aldoase reductase-like genes."
 Eur. J. Biochem. 259:726-730 (1999).

[6] SEQUENCE FROM N.A.
 STRAIN=BALB/c;
 MEDLINE=99160426; PubMed=10049784;
 Li H., Nobukuni Y., Gui T., Yabe-Nishimura C.;
 "Characterization of genomic regions directing the cell-specific expression of the mouse aldoase reductase gene."
 Biochem. Biophys. Res. Commun. 255:759-764 (1999).

[7] SEQUENCE FROM N.A.
 TISSUE=Breast;
 MEDLINE=22388257; PubMed=12477932;
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Udén T.B., Toshyiki S., Carinci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shcherenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
 Proc. Natl. Acad. Sci. U.S.A. 99:15699-15693 (2002).

-!- FUNCTION: Catalyzes the NADPH-dependent reduction of a wide variety of carbonyl-containing compounds to their corresponding alcohols with a broad range of catalytic efficiencies.

-!- CATALYTIC ACTIVITY: Alditol + NAD(P)(+) = aldose + NAD(P)H.

-!- SUBUNIT: Monomer.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- TISSUE SPECIFICITY: Abundant in the testis, skeletal muscle and kidney.
 CC -!- SIMILARITY: Belongs to the aldo/keto reductase family.
 CC
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 CC
 CC EMBL; D32250; BAA06980.1; -
 CC EMBL; L39795; AAA62176.1; -
 CC EMBL; U29152; AAA69958.1; -
 CC EMBL; U89150; AAC13358.1; -
 CC EMBL; U89140; AAC13358.1; JOINED.
 CC EMBL; U89142; AAC13358.1; JOINED.
 CC EMBL; U89143; AAC13358.1; JOINED.
 CC EMBL; U89144; AAC13358.1; JOINED.
 CC EMBL; U89145; AAC13358.1; JOINED.
 CC EMBL; U89146; AAC13358.1; JOINED.
 CC EMBL; U89147; AAC13358.1; JOINED.
 CC EMBL; U89148; AAC13358.1; JOINED.
 CC EMBL; U89149; AAC13358.1; JOINED.
 CC EMBL; U93231; AAD32300.1; -
 CC EMBL; U93230; AAD32300.1; JOINED.
 CC EMBL; AB016665; BAA76413.1; -
 CC EMBL; AB016662; BAA76413.1; JOINED.
 CC EMBL; AB016663; BAA76413.1; JOINED.
 CC EMBL; AB016664; BAA76413.1; JOINED.
 CC EMBL; BC004725; AAH04725.1; -
 CC EMBL; BC021655; AAH21655.1; -
 CC F01; I49484; I49484.
 CC HSP; P15121; 2ACQ.
 CC PMMA-2DPAGE; P45376; MOUSE.
 CC MGD; MGI:1353494; Akribi.
 CC InterPro: IPR001395; Aldo/ket_red.
 CC Pfam: PF00248; aldo_ket_red; 1.
 CC PRINTS; PR00089; ALDOKETREDTASE.
 CC ProDom; PD000288; Aldo/ket_red; 1.
 CC PROSITE; PS00062; ALDOKETO_REDUCTASE_2; 1.
 CC PROSITE; PS00063; ALDOKETO_REDUCTASE_3; 1.
 CC PROSITE; PS00798; ALDOKETO_REDUCTASE_1; 1.
 CC Oxidoreductase; NADP; acetylation; Multigene family.
 KW INIT_MET 0 0 BY SIMILARITY:
 FT NP_BIND 9 18 NADP (POTENTIAL).
 FT ACT_SITE 48 48 HYDROGEN-BOND DONOR (BY SIMILARITY).
 FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
 FT CONFLICT 45 45 A -> S (IN REF. 1).
 FT CONFLICT 220 220 A -> G (IN REF. 4).
 FT CONFLICT 280 280 V -> L (IN REF. 7).
 SQ SEQUENCE 315 AA; 35601 MW; 607E604FF432580E CRC64;
 Query Match 36.2%; Score 44.5; DB 1; Length 315;
 Best Local Similarity 41.2%; Pred. No. 15;
 Matches 7; Conservative 4; Mismatches 5; Indels 1; Gaps 1;
 QY 2 NWRCCILIPACRNHKKF 18
 DB 294 NWRVCAIMSCAK-HDY 309
 RESULT 19
 ALDR RAT
 ID ALDR RAT STANDARD; PRT; 315 AA.
 AC P07943;
 DT 01-NOV-1988 (Rel. 08, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Aldoase reductase (EC 1.1.1.21) (AR) (Aldohyde reductase).

AKR1B1 OR ALDR1.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;

SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN=Sprague-Dawley; TISSUE=Lens;
MEDLINE=87276556; PubMed=3111886;
Carter D., Nishimura C., Shinohara T., Dietzchold B., Wistow G.,
Craft C., Kador P., Kinoshita J.H.;
"Aldose reductase and p-crystallin belong to the same protein
superfamily as aldehyde reductase";
FEBS Lett. 220:209-213(1987).

SEQUENCE FROM N.A.
MEDLINE=92084118; PubMed=1748296;
Graham C.E., Szpirer C., Levan G., Carper D.,
"Characterization of the aldose reductase-encoding gene family in
rat.";
Gene 107:259-267(1991).

[3]
SEQUENCE OF 155-168 AND 204-209.
TISSUE=Astocytes;
MEDLINE=96007949; PubMed=7498172;
Laeng P., Bouillon P., Taupenot L., Labourdette G.;
"Long-term induction of an aldose reductase protein by basic
fibroblast growth factor in rat astrocytes in vitro.";
Electrophoresis 16:1240-1250(1995).
-!- FUNCTION: Catalyzes the NADPH-dependent reduction of a wide
variety of carbonyl-containing compounds to their corresponding
alcohols with a broad range of catalytic efficiencies.
-!- CATALYTIC ACTIVITY: Alditol + NAD(P)(+) = aldose + NAD(P)H.
-!- SUBUNIT: Monomer.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the aldol/keto reductase family.

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or send an email to license@isb-sib.ch).

EMBL; X05884; CAA29308.1; --
EMBL; M60322; AAA40721.1; --
PIR; A60603; A60603.
HSP; P15121; ZACQ.
InterPro; IPR001395; Aldo/ket_red.
Pfam; PF00248; aldo_ket_red; 1.
PRINTS; PR00069; ALDKETRDTASE.
ProDom; PD000288; Aldo/ket_red; 1.
PROSITE; PS00062; ALDOKETO_REDUCTASE_2; 1.
PROSITE; PS00063; ALDOKETO_REDUCTASE_3; 1.
PROSITE; PS00798; ALDOKETO_REDUCTASE_1; 1.
Oxidoreductase; NADP; Acetylation.
INIT MET 0 BY SIMILARITY.
NP BIND 9 18 NADP (POTENTIAL).
ACT SITE 48 48 HYDROGEN-BOND DONOR (BY SIMILARITY).
MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
SEQUENCE 315 AA; 35666 MW; 572941A154BC1202 CRC64;

Query Match 36.2%; Score 44.5; DB 1; Length 315;
Best local Similarity 41.2%; Pred. No. 15;
Matches 7; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

2 NWRCCLPACRRNHKFP 18
|||
294 NWRVCALMSCAK-HKYD 309

SULT 20

TAGC DICI1 STANDARD; PRT; 1743 AA.
ID TAGC DICI1 AC Q23858;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Prestalk-specific protein tagC precursor (EC 3.4.21.-).
GN TAGC.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]_taxid=44689;
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RX MEDLINE=97140317; PubMed=8986798;
RT Shaulsky G., Escalante R., Loomis W.F.;
"Developmental signal transduction pathways uncovered by genetic
suppressors.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:15260-15265(1996).
CC -!- FUNCTION: Intercellular communication via tagC may mediate
integration of cellular differentiation with morphogenesis (By
similarity).
CC -!- SIMILARITY: In the N-terminal section; belongs to peptidase family
S8.
CC -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE ATP-BINDING
TRANSPORT PROTEIN FAMILY (ABC TRANSPORTERS). MDR SUBFAMILY.
CC -!- SIMILARITY: STRONG, TO TAGB.

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or send an email to license@isb-sib.ch).

EMBL; U60866; AAB03331.1; --
PIR; T18279; T18279.
DictyBase; DB0001795; tagC.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR001140; ABC_TM_transp.
InterPro; IPR003439; ABC_transporter.
InterPro; IPR000209; Peptidase_S8.
Pfam; PF00664; ABC_membrane; 1.
Pfam; PF00005; ABC_tran; 1.
Pfam; PF00082; Peptidase_S8; 1.
PRINTS; PR00723; SUBTILISIN.
SMART; SM00382; AAA; 1.
PROSITE; PS50929; ABC_TM1F; 1.
PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
PROSITE; PS00136; SUBTILASE_ASP; FALSE_NEG.
PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_SER; FALSE_NEG.
KW Hydrolase; Serine protease; ATP-binding; Transport; Transmembrane;
Signal.
FT CHAIN 1 27 POTENTIAL.
FT DOMAIN 28 1743 PRESTALK-SPECIFIC PROTEIN TAGC.
FT DOMAIN 316 642 PROTEASE.
FT DOMAIN 1450 1687 ABC_TRANSPORTER.
FT TRANSMEM 962 982 POTENTIAL.
FT TRANSMEM 1027 1047 POTENTIAL.
FT TRANSMEM 1072 1092 POTENTIAL.
FT TRANSMEM 1157 1177 POTENTIAL.
FT TRANSMEM 1260 1280 POTENTIAL.
FT TRANSMEM 1288 1308 POTENTIAL.
FT ACT_SITE 325 325 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 372 372 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 637 637 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT NP_BIND 1485 1492 ATP (POTENTIAL).
FT DOMAIN 42 46 POLY-ASN.
FT DOMAIN 94 103 POLY-ASN.
FT DOMAIN 643 646 POLY-ALA.

DOMAIN 733 741 POLY-ASN.
 DOMAIN 786 792 POLY-SER.
 DOMAIN 1337 1340 POLY-GLU.
 DOMAIN 1346 1352 POLY-GLY.
 DOMAIN 1353 1357 POLY-ASP.
 DOMAIN 1358 1364 POLY-ASP.
 DOMAIN 1381 1386 POLY-ASN.
 DOMAIN 1707 1729 POLY-ASN.
 CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 536 536 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 547 547 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 689 689 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 735 735 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 741 741 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 776 776 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 832 832 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 887 887 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 1251 1251 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 1385 1385 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 1386 1386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 1454 1454 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 1704 1704 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SEQUENCE 1743 AA; 12DB363E2F29839 CRC64;
 Query Match 36.2%; Score 44.5; DB 1; Length 1743;
 Best Local Similarity 40.9%; Pred. No. 75;
 Matches 9; Conservative 2; Mismatches 6; Indels 5; Gaps 1;
 3 WRCCLPACRRNH-----KKFC 19
 933 WSCCLIQSCDNNYNSIKKFC 954

SULT 21
 A1_CONEP STANDARD; PRT; 16 AA.
 P56638;
 15-DEC-1998 (Rel. 37, Created)
 15-DEC-1998 (Rel. 37, Last sequence update)
 28-FEB-2003 (Rel. 41, Last annotation update)
 Alpha-conotoxin Epi.
 Conus episcopatus (Bishop's cone).
 Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 Neogastropoda; Conoidea; Conidae; Conus.
 NCBI_TaxID=88764;
 [1]
 X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
 MEDLINE=98376423; PubMed=9708977;
 Fu S.H., Loughnan M., Miller R., Weeks C.M., Blessing R.H.,
 Alewood P.F., Lewis R.J., Martin J.L.;
 "The 1.1-A resolution crystal structure of [Tyr15]Epi, a novel
 alpha-conotoxin from Conus episcopatus, solved by direct methods.";
 Biochemistry 37:11425-11433(1998).
 -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
 bind to the nicotinic acetylcholine receptors (nAChR) and thus
 inhibit them. This peptide blocks mammalian nicotinic
 acetylcholine receptors composed of alpha-3/beta-2 and alpha-
 3/beta-4 subunits.
 -!- SUBCELLULAR LOCATION: Secreted.
 -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
 family.
 PIR; A59042; A59042.
 PDB; 1A0M; 13-JAN-99.
 Postsynaptic neurotoxin; Neurotoxin; Toxin;
 Acetylcholine receptor inhibitor; Amidation; 3D-structure.
 Sulfation; 3D-structure.
 DISULFID 2 8
 DISULFID 3 16
 MOD_RES 15 15 SULFATION.
 MOD_RES 16 16 AMIDATION.

FT HELIX 2 4
 FT HELIX 6 11
 FT TURN 13 16
 SQ SEQUENCE 16 AA; 1792 MW; C63385F376C99B4C CRC64;
 Query Match 35.8%; Score 44; DB 1; Length 16;
 Best Local Similarity 40.0%; Pred. No. 1;
 Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
 QY 5 CCLIPACRRNHKKFC 19
 DB 2 CCSDPRCNMNPDYC 16
 RESULT 22
 CXA2_CONNA STANDARD; PRT; 16 AA.
 ID_CXA2_CONNA STANDARD; PRT; 16 AA.
 AC P56636;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alpha-conotoxin MII (M2).
 OS Conus magus (Magus cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6492;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Venom;
 RX MEDLINE=96205934; PubMed=8631783;
 RA Cartier G.E., Yoshikami D., Gray W.R., Luo S., Olivera B.M.,
 RA McIntosh J.M.;
 RT "A new alpha-conotoxin which targets alpha3beta2 nicotinic
 acetylcholine receptors.";
 RL J. Biol. Chem. 271:7522-7528(1996).
 RN [2]
 RP STRUCTURE BY NMR.
 RX MEDLINE=98062282; PubMed=9398298;
 RA Shon K.-J., Koerber S.C., Rivier J.E., Olivera B.M., McIntosh J.M.;
 RT "Three-dimensional solution structure of alpha-conotoxin MII, an
 alpha3beta2 neuronal nicotinic acetylcholine receptor-targeted
 ligand.";
 RL Biochemistry 36:15693-15700(1997).
 RN [3]
 RP STRUCTURE BY NMR.
 RX MEDLINE=99060038; PubMed=9843365;
 RA Hill J.M., Oomen C.J., Miranda L.P., Bingham J.-P., Alewood P.F.,
 RA Craik D.J.;
 RT "Three-dimensional solution structure of alpha-conotoxin MII by NMR
 spectroscopy: effects of solution environment on helicity.";
 RL Biochemistry 37:15621-15630(1998).
 CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
 bind to the nicotinic acetylcholine receptors (nAChR) and thus
 inhibit them. This peptide blocks mammalian nicotinic
 acetylcholine receptors composed of alpha-3/beta-2 subunits. It
 has an activity 2 to 4 orders of magnitude less potent on other
 nAChR subunit combinations.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
 family.
 PIR; A59046; A59046.
 PDB; 1MII; 21-OCT-98.
 PDB; 1M2C; 13-JAN-99.
 Postsynaptic neurotoxin; Neurotoxin; Toxin;
 Acetylcholine receptor inhibitor; Amidation; 3D-structure.
 FT DISULFID 2 8
 FT DISULFID 3 16 AMIDATION.
 FT MOD_RES 16 16
 FT TURN 2 4
 FT TURN 7 11
 FT TURN 12 16

SEQUENCE 16 AA; 1716 MW; 282AEF190166CAF9 CRC64;
Query Match 35.8%; Score 44; DB 1; Length 16;
Best Local Similarity 40.0%; Pred. No. 1; Mismatches 0; Gaps 0;
Matches 6; Conservative 0; Indels 9;
5 CCLIPACRRNHKKFC 19
|||
2 CCNPNVCHLEHSLC 16
SULT 23
31 SCHPO STANDARD; PRT; 271 AA.
RCCL SCHPO
094448;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable CAAX prenyl protease 2 (EC 3.4.22.-) (Prenyl protein-specific
endoprotease 2) (PPSEP 2).
SPAC1687.02.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomycetes.
NCBI_TaxID=4896;
[1]
SEQUENCE FROM N.A.
STRAIN=972;
MEDLINE=21848401; PubMed=11859360;
Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
Sgouros J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
Gentles S., Godle A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
Skilton J., Simmonds M., Squares R., Squares K., Stevens K.,
Taylor K., Taylor R.G., Rivey A., Walsh S.V., Warren T., Whitehead S.,
Woodward J., Voiclaert G., Aert R., Robben J., Grymonprez B.,
Waltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
Eger P., Zimmermann W., Wedler H., Wamburt R., Purnelle B.,
Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe";
Nature 415:871-880(2002).
-!- FUNCTION: Proteolytically removes the C-terminal three residues of
farnesylated proteins (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
reticulum (By similarity).
-!- SIMILARITY: Belongs to peptidase family U48.

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EMBL; AL035064; CAA22596.1; -
PIR; T37745; T37745.
MEROPS; U48.UPW; -

DR GenDB SPombe; SPAC1687.02; -.
DR InterPro; IPR003675; Abi.
DR Pfam; PF02517; Abi.1
KW Hypothetical protein; Hydrolase; Transmembrane; Endoplasmic reticulum.
FT TRANSMEM 3 23 POTENTIAL.
FT TRANSMEM 42 62 POTENTIAL.
FT TRANSMEM 174 194 POTENTIAL.
FT TRANSMEM 236 256 POTENTIAL.
SQ SEQUENCE 271 AA; 31024 MW; 7274E9BE25348BB CRC64;
Query Match 35.8%; Score 44; DB 1; Length 271;
Best Local Similarity 55.6%; Pred. No. 15; Mismatches 3; Indels 0; Gaps 0;
Matches 5; Conservative 3;
QY 3 WRCLIPAC 11
|||
DB 130 FRCCIVPIC 138
RESULT 24
ALD2 MOUSE STANDARD; PRT; 315 AA.
ID ALD2 MOUSE
AC P45377;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Aldose reductase-related protein 2 (EC 1.1.1.21) (AR) (Aldehyde
reductase) (Fibroblast growth factor regulated protein) (FR-1
protein).
DE protein.
GN AKR1B8 OR FGFRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=94179253; PubMed=7510692;
RA Donohue P.J., Alberts G.F., Hampton B.S., Winkles J.A.;
"A delayed-early gene activated by fibroblast growth factor-1 encodes
a protein related to aldose reductase";
J. Biol. Chem. 269:8604-8609(1994).
[2]
RT X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
RN MEDLINE=96062495; PubMed=7578036;
RX Wilson D.K., Nakano T., Petrash M., Quirocho F.A.;
"1.7-A structure of FR-1, a fibroblast growth factor-induced member
of the aldo-keto reductase family, complexed with coenzyme and
inhibitor";
Biochemistry 34:14323-14330(1995).
RL Biochemistry 34:14323-14330(1995).
CC -!- CATALYTIC ACTIVITY: Alditol + NAD(P) (+) = aldose + NAD(P)H.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- INDUCTION: By FGF-1.
CC -!- SIMILARITY: Belongs to the aldo/keto reductase family.

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EMBL; U04204; AAA16953.1; -
DR PIR; A53440; A53440.
DR PDB; 1FRB; 14-OCT-96.
DR MGD; MGI:107673; Akrlb8.
DR InterPro; IPR001395; Aldo/ket red.
DR Pfam; PF00248; aldo_ket_red; 1.
DR PRINTS; PR00069; ALDKETREDTASE.
DR ProDom; PD000288; Aldo/ket_red; 1.
DR PROSITE; PS00062; ALDO-KETO_REDUCTASE_2; 1.

PROSITE; PS00063; ALDO-KETO REDUCTASE 3; 1.
PROSITE; PS00798; ALDO-KETO REDUCTASE 1; 1.
Oxidoreductase; NADP; Multigene family; 3D-structure.
INIT MET 0 0
ACT SITE 48 48
STRAND 3 5
TURN 7 8
STRAND 11 13
STRAND 15 15
STRAND 17 18
TURN 20 21
HELEX 24 36
TURN 37 38
STRAND 41 43
HELEX 46 48
TURN 49 49
HELEX 51 63
TURN 64 65
HELEX 69 71
STRAND 73 78
HELEX 80 82
HELEX 85 99
TURN 100 100
STRAND 104 109
STRAND 115 115
STRAND 124 124
TURN 126 127
STRAND 130 130
STRAND 132 132
HELEX 137 149
TURN 150 151
STRAND 153 159
HELEX 163 170
TURN 171 171
TURN 173 174
STRAND 181 185
STRAND 187 187
TURN 188 189
STRAND 190 190
HELEX 193 201
TURN 202 203
STRAND 205 209
TURN 211 212
TURN 215 216
TURN 218 219
TURN 222 223
TURN 227 229
HELEX 231 239
TURN 240 241
HELEX 244 253
TURN 254 256
STRAND 258 259
STRAND 262 262
HELEX 266 273
HELEX 282 289
TURN 290 291
HELEX 301 303
TURN 304 305
TURN 307 308
TURN 311 312
SEQUENCE 315 AA; 35989 MW; 8D9633994A3F5B7C CRC64;

Query Match 35.8%; Score 44; DB 1; Length 315;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

2 NWRCCCLIP 9

294 NWRACLLP 301

SULT 25
DH_AME

ID FADH_AMEYME STANDARD; PRT; 360 AA.
AC PS0094;
DT 01-DEC-1992 (Rel. 24, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE NAD/mycothiol-dependent formaldehyde dehydrogenase (EC 1.2.1.66) (MD-FALDH)
DE FALDH
OS Amycolatopsis methanolica.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Pseudonocardiaceae; Pseudonocardiaceae; Amycolatopsis.
NCBI_TaxID=1814;
RN [1]
RP SEQUENCE.
RX MEDLINE=98004265; PubMed=9346279;
RA Norin A., van Ophem P.W., Piersma S.R., Persson B., Duine J.A., Joernvall H.;
RA "Mycothiol-dependent formaldehyde dehydrogenase, a prokaryotic medium-chain dehydrogenase/reductase, phylogenetically links different eukaryotic alcohol dehydrogenases -- primary structure, conformational modelling and functional correlations.";
RL Eur. J. Biochem. 248:282-289(1997).
RN [2]
RP PRELIMINARY SEQUENCE OF 1-31.
RX MEDLINE=92283278; PubMed=1597190;
RA van Ophem P.W., van Beesmen J., Duine J.A.;
RT "NAD-linked, factor-dependent formaldehyde dehydrogenase or trimeric, zinc-containing, long-chain alcohol dehydrogenase from Amycolatopsis methanolica";
RL Eur. J. Biochem. 206:511-518(1992).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=97345657; PubMed=9202149;
RA Misset-Smits M., van Ophem P.W., Sakuda S., Duine J.A.;
RT "Mycothiol, 1-O-(2'-[N-acetyl-L-cysteinyllamido-2'-deoxy-alpha-D-glucopyranosyl)-D-myo-inositol, is the factor of NAD/factor-dependent formaldehyde dehydrogenase.";
RL FEBS Lett. 409:221-222(1997).
CC -!- CATALYTIC ACTIVITY: Formaldehyde + mycothiol + NAD(+) = S-formylmycothiol + NADH.
CC -!- COFACTOR: Binds 2 zinc ions per subunit (By similarity).
CC -!- SUBUNIT: Homotrimer.
CC -!- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase family.
DR InterPro; IPR003228; ADH_zinc.
DR InterPro; IPR002085; Adh_zn_family.
DR InterPro; IPR00205; NAD_BS.
DR Pfam; PF00107; ADH_zinc_N; 1.
DR PROSITE; PS00059; ADH_ZINC; 1.
KW Oxidoreductase; Zinc; Metal-binding; NAD.
FT ACT SITE 89 89 SUBSTRATE BINDING (PROBABLE).
FT METAL 41 41 ZINC 1 (CATALYTIC) (BY SIMILARITY).
FT METAL 62 62 ZINC 1 (CATALYTIC) (BY SIMILARITY).
FT METAL 92 92 ZINC 2 (BY SIMILARITY).
FT METAL 95 95 ZINC 2 (BY SIMILARITY).
FT METAL 98 98 ZINC 2 (BY SIMILARITY).
FT METAL 106 106 ZINC 2 (BY SIMILARITY).
FT METAL 161 161 ZINC 1 (CATALYTIC) (BY SIMILARITY).
SQ SEQUENCE 360 AA; 37757 MW; 48BED1F70EAB2CE7 CRC64;

Query Match 35.8%; Score 44; DB 1; Length 360;
Best Local Similarity 40.0%; Pred. No. 20;
Matches 8; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

QY 2 NWR--CCLIPACRENHKKFC 19

DB 87 NWRVCGGCRACKGRQPYC 106

RESULT 26

SEC5 HUMAN

ID SEC5 HUMAN STANDARD; PRT; 924 AA.

AC Q96RF1; Q96ANG; Q9NUZ8; Q9UJW7;

DT 28-FEB-2003 (Rel. 41, Created)

28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Exocyst complex component Sec5.

SEC5 OR SEC5L1

Homo sapiens (Human)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;

[1] SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND INTERACTION WITH GNEFR.
MEDLINE=22347268; PubMed=12459492;

Sjoelinder M., Uhlmann J., Ponstingl H.;

"DELGF", a homologue of the Ran guanine nucleotide exchange factor
RANGF, binds to the exocyst component Sec5 and modulates secretion."
FEBS Lett. 532:211-215 (2002).

[2] SEQUENCE OF 1-793 FROM N.A.

Whitaker H.;

Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

[3] SEQUENCE OF 119-924 FROM N.A.

TISSUE=Brain;

MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
Bosak S.A., Mcwan P.J., Kerner K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
Fanev J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[4] SEQUENCE OF 143-924 FROM N.A.

TISSUE=Placenta;

Isoqai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,
Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;

"NEDO human cDNA sequencing project.";

Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

-!- FUNCTION: Component of the exocyst complex involved in the docking
of exocystic vesicles with fusons site on the plasma membrane.

-!- SUBUNIT: The exocyst complex is composed of SEC3, SEC5, SEC6,
SEC8, SEC10, SEC15, EXO70 and EXO84. Interacts with RALA and
GNEFR/DELGF. Interaction with GNEFR occurs only in the presence
of magnesium or manganese and is stimulated by dCTP or GTP.

-!- TISSUE SPECIFICITY: Widely expressed with highest levels in brain
and placenta.

-!- DOMAIN: Interacts with RALA through the TIG domain (By

similarity).

-!- SIMILARITY: Belongs to the SEC5 family.

-!- SIMILARITY: Contains 1 TIG domain.

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send an email to license@isb-sib.ch).

DR EMBL; AJ414403; CAC92092.1; -;
DR EMBL; AL031770; -; NOT ANNOTATED CDS.
DR EMBL; BC016918; AAH16918.1; ALT_INIT.
DR EMBL; AK001888; BAA91963.1; ALT_INIT.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR002909; IFT_TIG.
DR Pfam; PF01833; TIG; 1.
KW Exocytosis; Transport; Protein transport; Coiled coil.
FT DOMAIN 8 93
FT DOMAIN 240 260 COILED COIL (POTENTIAL).
FT CONFLICT 522 522 L -> H (IN REF. 4).
SQ SEQUENCE 924 AA; 104066 MW; 2234E463D8B076F CRC64;
Query Match 35.8%; Score 44; DB 1; Length 924;
Best Local Similarity 47.1%; Pred. NO. 49;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 1 FNRCCCLIPACRRNHKK 17
DB 784 FDKKCLPPTGVRNLYK 800
RESULT 27
ALDR FIG
ID ALDR FIG STANDARD; PRT; 315 AA.
AC P80276;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Aldose reductase (EC 1.1.1.21) (AR) (Aldohyde reductase).
GN AKR1B1 OR ALR2.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
RN [1]
RP SEQUENCE, MASS SPECTROMETRY, AND DISULFIDE BOND.
RC TISSUE=Lens;
RX MEDLINE=94109388; PubMed=8281941;
RA Jaquinod M., Potier N., Klarskov K., Reyman J.-M., Sorokine O.,
RA Kieffer S., Barth P., Andrianomanga V., Biellmann J.-F.,
RA van Dorsselaer A.;
RA "Sequence of pig lens aldose reductase and electrospray mass
spectrometry of non-covalent and covalent complexes.";
Eur. J. Biochem. 218:893-903 (1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93263021; PubMed=8493902;
RA Kubieski T.J., Green N.C., Flynn T.G.;
RA "Location of an essential arginine residue in the primary structure
of pig aldose reductase.";
Adv. Exp. Med. Biol. 328:259-265 (1993).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=92131138; PubMed=1734286;
RA Rondeau J.-M., Tete-Favre F., Podjarny A., Reyman J.-M., Barth P.,
RA Biellmann J.-F., Moras D.;
RA "Novel NADPH-binding domain revealed by the crystal structure of
aldose reductase.";
Nature 355:469-472 (1992).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=97341224; PubMed=9195881;
RA Urzhumteev A., Tete-Favre F., Mitschler A., Baranton J., Barth P.,
RA Urzhumteeva L., Biellmann J.-F., Podjarny A.D., Moras D.;
RA "A 'specificity' pocket inferred from the crystal structures of the
complexes of aldose reductase with the pharmacologically important
inhibitors tolrestat and sorbinil.";
Structure 5:601-612 (1997).
CC -!- FUNCTION: Catalyzes the NADPH-dependent reduction of a wide
variety of carbonyl-containing compounds to their corresponding
alcohols with a broad range of catalytic efficiencies.

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EMBL; U13694; AAB60687.1; -.
 EMBL; U13689; AAB60687.1; JOINED.
 EMBL; U13690; AAB60687.1; JOINED.
 EMBL; U13691; AAB60687.1; JOINED.
 EMBL; U13692; AAB60687.1; JOINED.
 EMBL; U13693; AAB60687.1; JOINED.
 EMBL; M32818; AAA31160.1; -.
 EMBL; U12316; AAA50833.1; -.
 EMBL; J05048; AAA31157.1; -.
 PIR; A34406; A34406.
 HSP; P15121; 2AC0.
 InterPro: IPR001395; Aldo/ket red.
 Pfam: PF00248; aldo_ket_red; 1.
 PRINTS; PR00069; ALDKETREDASE.
 ProDom; PD000288; Aldo/ket_red; 1.
 PROSITE; PS00062; ALDOKETO REDUCTASE_2; 1.
 PROSITE; PS00063; ALDOKETO REDUCTASE_3; 1.
 PROSITE; PS00798; ALDOKETO REDUCTASE_1; 1.
 Oxidoreductase; NADP; Acetylation.
 INIT MET 0 BY SIMILARITY.
 NP_BIND 9 18 NADP (POTENTIAL).
 ACT_SITE 48 48 HYDROGEN-BOND DONOR (BY SIMILARITY).
 MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
 SEQUENCE 315 AA; 35632 MW; 64D53E6AC0853FFB CRC64;

Query Match 35.4%; Score 43.5; DB 1; Length 315;
 Best Local Similarity 41.2%; Pred. No. 21;
 Matches 7; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

2 NWRCCCLIPACRHNKX 18

294 NWRVCALVSC-ASHKDY 309

SULT 29

F_DROME DROME STANDARD; PRT; 797 AA.
 Q24472;
 30-MAY-2000 (Rel. 39, Created)
 30-MAY-2000 (Rel. 39, Last sequence update)
 30-MAY-2000 (Rel. 39, Last annotation update)
 Retinoblastoma-family protein.
 RBF.
 Drosophila melanogaster (Fruit fly).
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 [1].

SEQUENCE FROM N.A.
 MEDLINE=96217922; PubMed=8675008;
 Du W., Vidal M., Xie J.-E., Dyson M.;
 "RBF, a novel RB-related gene that regulates E2F activity and
 interacts with cyclin E in Drosophila.";
 Genes Dev. 10:1206-1218(1996).
 -!- FUNCTION: Functions in cell cycle regulation. Potent inhibitor of
 E2F-mediated transactivation.
 -!- SUBUNIT: Forms a complex with the DRP1/E2F transcription factor
 through binding to a C-terminal region of E2F. This binding
 inhibits the E2F-mediated transactivation activity.
 -!- SUBCELLULAR LOCATION: Nuclear.
 -!- PTM: PHOSPHORYLATION BY CYCLIN-E-DEPENDENT KINASES APPEARS TO
 NEGATIVELY REGULATE RBF ACTIVITY.
 -!- SIMILARITY: Belongs to the retinoblastoma protein (RB) family.

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EMBL; X96975; CAA65661.1; -.
 HSSP; P06400; IGUX.
 FlyBase: FBgn0015799; Rbf.
 GO; GO:008285; P:negative regulation of cell proliferation; NAS.
 InterPro: IPR006670; Cyclin.
 InterPro: IPR002720; RB A.
 InterPro: IPR002719; RB_B.
 Pfam; PF01859; RB_A; 1.
 Pfam; PF01857; RB_B; 1.
 SMART; SM00385; CYCLIN; 1.
 KW Transcription regulation; DNA-binding; Nuclear protein; Cell cycle;
 Phosphorylation.
 FT DOMAIN 374 711 POCKET.
 FT DOMAIN 374 566 DOMAIN A.
 FT DOMAIN 576 711 DOMAIN B.
 SQ SEQUENCE 797 AA; 91910 MW; SEA0C4638A677303 CRC64;

Query Match 35.4%; Score 43.5; DB 1; Length 797;
 Best Local Similarity 61.5%; Pred. No. 50;
 Matches 8; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 2 NWRCCCLIPACR 13

DB 68 HWMCCAIYACRR 80

RESULT 30

JAG1_HUMAN
 ID JAG1_HUMAN STANDARD; PRT; 1218 AA.
 AC P78504; O14902; O15122; Q15816;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Jagged 1 precursor (Jagged1) (hJ1).
 GN JAG1 OR JAGL1
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97422615; PubMed=9268641;
 RA Oda T., Elkahoun A.G., Meltzer P.S., Chandrasekharappa S.C.;
 "Identification and cloning of the human homolog (JAG1) of the rat
 Jagged1 gene from the Alagille syndrome critical region at 20p12.";
 RL Genomics 43:376-379(1997).
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANT AGS CYS-184.
 RC TISSUE=Bone marrow;
 RX MEDLINE=97351506; PubMed=9207788;
 RA Li L., Krantz I.D., Deng Y., Genin A., Banta A.B., Collins C.C.,
 Qi M., Trask B.J., Kuo W.L., Cochran J., Costa T., Pierpont M.E.M.,
 Rand E.B., Piccoli D.A., Hood L., Spinner N.B.;
 "Alagille syndrome is caused by mutations in human Jagged1, which
 encodes a ligand for Notch1.";
 RT Nat. Genet. 16:243-251(1997).
 RN [3]
 RP SEQUENCE FROM N.A., AND FUNCTION.
 RX MEDLINE=98122342; PubMed=9462510;
 RA Li L., Milner L.A., Deng Y., Iwata M., Banta A.B., Graf L.,
 Marcovina S., Friedman C., Trask B.J., Hood L., Torok-Storb B.;
 "The human homolog of rat Jagged1 expressed by marrow stroma inhibits
 differentiation of 32D cells through interaction with Notch1.";
 RT Immunity 8:43-55(1998).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cervical carcinoma;

- MEDLINE=99262417; PubMed=10329626;
 Bash J., Zong W.-X., Barga S., Rivera A., Ballard D.W., Ron Y.,
 Celinas C.;
 "Rel/NF-kappaB can trigger the Notch signaling pathway by inducing the
 expression of Jagged1, a ligand for Notch receptors.";
 EMBO J. 18:2803-2811(1999).
 [5]
 SEQUENCE FROM N.A.
 MEDLINE=99180765; PubMed=10079256;
 Gray G.E., Mann R.S., Mitsiadis E.;
 Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;
 "Human ligands of the Notch receptor.";
 Am. J. Pathol. 154:785-794(1999).
 [6]
 SEQUENCE FROM N.A.
 MEDLINE=21638749; PubMed=11780052;
 Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.L.,
 Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 Coulson A., Coville G.J., Deadman R., Dharm P.D., Dunn M.,
 Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 Grahnam D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 Hammond S., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.K., Johnson D.,
 Huckle E., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 Leharvalho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 Marsh V.L., Martin S.L., McConachie L.J., McLay K., Murrill A.A.,
 Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ransay H.,
 Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
 Skuse C.D., Smith M.B., Soderlund C., Steward C.A., Sturton J.E.,
 Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 Rogers J.;
 "The DNA sequence and comparative analysis of human chromosome 20.";
 Nature 414:865-871(2001).
 [7]
 SEQUENCE OF 14-1227 FROM N.A.
 TISSUE=Umbilical vein endothelial cells;
 MEDLINE=97115768; PubMed=8955070;
 Zimin A.B., Pepper M.S., McMahon G.A., Nguyen F., Montesano R.,
 Maciag T.;
 "an antisense oligonucleotide to the notch ligand jagged enhances
 fibroblast growth factor-induced angiogenesis in vitro.";
 J. Biol. Chem. 271:32499-32502(1996).
 [8]
 DISBASE.
 MEDLINE=97351505; PubMed=9207787;
 Oda T., Elkahoul A.G., Pike B.L., Okajima K., Krantz I.D., Genin A.,
 Piccoli D.A., Meltzer P.S., Spinner N.B., Collins F.S.,
 Chandrasekharappa S.C.;
 "Mutations in the human Jagged1 gene are responsible for Alagille
 syndrome.";
 Nat. Genet. 16:235-242(1997).
 [9]
 DEVELOPMENTAL STAGE.
 MEDLINE=20436345; PubMed=10979356;
 Jones E.A., Clement-Jones M., Wilson D.I.;
 "JAGGED1 expression in human embryos: correlation with the Alagille
 syndrome phenotype.";
 J. Med. Genet. 37:663-668(2000).
 [10]
 VARIANTS AGS CYS-184 AND HIS-184.
 MEDLINE=98254456; PubMed=98585603;
 Krantz I.D., Colliton R.P., Genin A., Rand E.B., Li L., Piccoli D.A.,
 Spinner N.B.;
 "Spectrum and frequency of jagged1 (JAG1) mutations in Alagille
 syndrome patients and their families.";
 Am. J. Hum. Genet. 62:1361-1369(1998).
 [11]
 VARIANTS AGS HIS-79; THR-127; ARG-129; LEU-163; GLY-184; SER-187;
 GLY-229; PHE-284; CYS-288; PHE-438; SER-731 AND ARG-740.
 MEDLINE=99238889; PubMed=1020506;
 Crosnier C., Briancourt C., Raynaud N., Phorne-Pollet S., Polet N.,
 Bernard O., Hadchouel M., Meunier-Rotival M.;
 "Mutations in JAGGED1 gene are predominantly sporadic in Alagille
 syndrome.";
 Gastroenterology 116:1141-1148(1999).
 [12]
 VARIANTS AGS THR-152 AND LEU-184.
 MEDLINE=20004539; PubMed=10533065;
 Piliya G., Uda M., Macis D., Frau F., Crisponi L., Balli F.,
 Barbera C., Colombo C., Frediani T., Gatti R., Iorio R., Marazzi M.G.,
 Marcellini M., Musumeci S., Nebbia G., Vajro P., Ruffa G., Zancan L.,
 Cao A., Devirgilis S.;
 "Jagged-1 mutation analysis in Italian Alagille syndrome patients.";
 Hum. Mutat. 14:394-400(1999).
 [13]
 VARIANTS AGS TYR-229 AND ARG-386.
 MEDLINE=20514559; PubMed=11058898;
 Heritage M.L., MacMillan J.C., Colliton R.P., Genin A., Spinner N.B.,
 Anderson G.J.;
 "Jagged1 (JAG1) mutation detection in an Australian Alagille syndrome
 population.";
 Hum. Mutat. 16:408-416(2000).
 [14]
 VARIANT TOF ASP-274.
 MEDLINE=21067871; PubMed=11152664;
 Eldadah Z.A., Hamosh A., Biery N.J., Montgomery R.A., Duke M.,
 Elkins R., Dietz H.C.;
 "Familial Tetralogy of Fallot caused by mutation in the jagged1
 gene.";
 Hum. Mol. Genet. 10:163-169(2001).
 [15]
 VARIANT AGS SER-37.
 MEDLINE=21096916; PubMed=11157803;
 Morissette J.D., Colliton R.P., Spinner N.B.;
 "Defective intracellular transport and processing of JAG1 missense
 mutations in Alagille syndrome.";
 Hum. Mol. Genet. 10:405-413(2001).
 [16]
 VARIANTS AGS PHE-220 AND ARG-753.
 MEDLINE=20579880; PubMed=11139247;
 Crosnier C., Briancourt C., Raynaud N., Hadchouel M.,
 Meunier-Rotival M.;
 "Fifteen novel mutations in the JAGGED1 gene of patients with Alagille
 syndrome.";
 Hum. Mutat. 17:72-73(2001).
 CC -!- FUNCTION: Ligand for multiple Notch receptors and involved in the
 CC mediation of Notch signaling. May be involved in cell-fate
 CC decisions during hematopoiesis. Seems to be involved in early
 CC and late stages of mammalian cardiovascular development. Inhibits
 CC myoblast differentiation (By similarity). Enhances fibroblast
 CC growth factor-induced angiogenesis (in vitro).
 CC -!- SUBUNIT: Interacts with NOTCH1, NOTCH2 AND NOTCH3 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC In cervix epithelium expressed in adult and fetal tissues.
 CC In reserve cells and squamous metaplasia. Expression is up-regulated
 CC in cervical squamous cell carcinoma. Expressed in bone marrow cell
 CC line HS-27a which supports the long-term maintenance of immature
 CC progenitor cells.
 CC -!- DEVELOPMENTAL STAGE: Expressed in 32-52 days embryos in the distal
 CC cardiac outflow tract and pulmonary artery, major arteries, portal
 CC vein, optic vesicle, otocyst, branchial arches, metanephros,
 CC pancreas, mesocardium, around the major bronchial branches, and in
 CC the neural tube.
 CC -!- DISEASE: Defects in JAG1 are the cause of Alagille syndrome (AGS)
 CC [MIM:118450]. AGS is an autosomal dominant development disorder

that affects structures in the liver, heart, skeleton, eye, kidney and other organs.

-I- DISEASE: Defects in JAG1 are a cause of tetralogy of Fallot (TOF) [MIM:187500]. TOF is a congenital heart anomaly which consists of pulmonary stenosis, ventricular septal defect, dextroposition of the aorta (aorta is on the right side instead of the left) and hypertrophy of the right ventricle. This condition results in a blue baby at birth due to inadequate oxygenation. Surgical correction is emergent.

-I- SIMILARITY: Contains 15 EGF-like domains.

-I- SIMILARITY: Contains 1 DSL domain.

-I- CAUTION: Ref.7 sequence differs from that shown due to a frameshift in position 1187.

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Query Match 35.4%; Score 43.5; DB 1; Length 1218;
Best Local Similarity 44.4%; Pred. No. 75;
Matches 8; Conservative 2; Mismatches 5; Indels 3; Gaps 1;

3 WRCLIPA---CRNHKK 17

|||||:|:|:|

1081 WICLVTAFFWCLRKRRK 1098

SULT 31

PS_BUCBP

ACPS_BUCBP STANDARD; PRT; 128 AA.

P59475;

10-OCT-2003 (Rel. 42, Created)

10-OCT-2003 (Rel. 42, Last sequence update)

10-OCT-2003 (Rel. 42, Last annotation update)

Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)

(4'-phosphopantetheinyl transferase acps).

ACPS OR BP237.

Buchnera aphidicola (subsp. Baizongia pistaciae).

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

Enterobacteriaceae; Buchnera.

NCBI_TaxID=135842;

[1]

SEQUENCE FROM N.A.

MEDLINE=22426901; PubMed=12522265;

Van Ham R.C.H.J., Kamerbeek J., Palacios C., Rausell C., Abascal F.,

Tastolla U., Fernandez J.M., Jimenez L., Postigo M., Silva F.J.,

Tanames J., Viguera E., Latorre A., Valencia A., Moran F., Moya A.;

"Reductive genome evolution in Buchnera aphidicola".

Proc. Natl. Acad. Sci. U.S.A. 100:581-586(2003).

-I- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme

A to a Ser of acyl-carrier protein (By similarity).

-I- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine

3',5'-bisphosphate + holo-[acyl-carrier protein].

-I- COFACTOR: Magnesium (By similarity).

-I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-I- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps

family.

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EMBL; AB014016; AAC026964.1; -

HAVAP; MF_00101; -; 1.

InterPro; IPR008278; 4-PPT transf.

InterPro; IPR002582; ACPS.

InterPro; IPR004568; Pantethn_trn.

Pfam; PF01648; ACPS; 1.

TIGRFAMs; TIGR00516; acps; 1.

TIGRFAMs; TIGR00556; pantethn_trn; 1.

Transferase; Lipid synthesis; pantethin; Fatty acid biosynthesis; Magnesium;

KW Complete proteome.
FT METAL 9
FT METAL 60
SQ SEQUENCE 128 AA; 14502 MW; 5ED8856BE07DDEDA CRC64;

Query Match 35.0%; Score 43; DB 1; Length 128;

Best Local Similarity 35.3%; Pred. No. 10;

Matches 6; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 2 NWRCLIPACRNHHKKF 18

:||:|:|:

Db 35 NYELNLEPCKNQYTKF 51

RESULT 32

FOL1_BOVIN

ID FOL1_BOVIN STANDARD; PRT; 222 AA.

AC P02702;

DT 21-JUL-1986 (Rel. 01, Created)

DT 23-OCT-1986 (Rel. 02, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Milk folate-binding protein (FBP) (Folate receptor alpha).

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OC NCBI_TaxID=9913;

RN [1]

RP SEQUENCE.

RC TISSUE=Milk;

RA Svendsen I., Hansen S.I., Holm J., Lyngbye J.;

RT "The complete amino acid sequence of the folate-binding protein from

cow's milk."

RL Carlsberg Res. Commun. 49:123-131(1984).

RN [2]

RP SEQUENCE OF 1-62; 72-102 AND 192-222.

RC TISSUE=Milk;

RA Svendsen I., Martin B., Pedersen T.G., Hansen S.I., Holm J.,

RA Lyngbye J.;

RT "Isolation and characterization of the folate-binding protein from

cow's milk."

RL Carlsberg Res. Commun. 44:89-99(1979).

CC -I- FUNCTION: Binds to folate and reduced folic acid derivatives and

mediates delivery of 5-methyltetrahydrofolate to the interior of

cells.

CC -I- PTM: Eight disulfide bonds are present.

CC -I- SIMILARITY: Belongs to the folate receptor family.

DR PIR; A03161; BFBO.

DR InterPro; IPR004269; Folt_chemrecept.

DR Pfam; PF03024; Folate_rec; 1. Folate-binding.

Receptor; Glycoprotein; Milk; N-LINKED (GLCNAC. . .).

FT CARBOHYD 49 49

FT CARBOHYD 141 141

FT SEQUENCE 222 AA; 25825 MW; 528C388E9A9C0484 CRC64;

Query Match 35.0%; Score 43; DB 1; Length 222;

Best Local Similarity 50.0%; Pred. No. 18;

Matches 8; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

QY 1 FNRWCC--LIPACREN 14

|||||:|:|:

Db 64 FNRDHCQKMEPACKEH 79

RESULT 33

YAT6_RHOBL

ID YAT6_RHOBL STANDARD; PRT; 249 AA.

AC P05439; C05939;

DT 01-NOV-1988 (Rel. 09, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE ATP synthase subunits region ORF 6.

OS Rhodospseudomonas blastica.

Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Rhodobacter.

NCBI_TaxID=1075;

[1]_SEQUENCE FROM N.A.

MEDLINE=85058188; PubMed=6209404;

Tybuliewicz V.L.J., Falk G., Walker J.E.;

"Rhodopseudomonas blattica atp operon. Nucleotide sequence and

transcription.";

J. Mol. Biol. 179:185-214(1984).

[2]

REVISION TO 164.

Tybuliewicz V.L.J., Falk G., Walker J.E.;

Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

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or send an email to license@isb-sib.ch).

EMBL: Z00018; CAA77302.1; -

PIR: S04674; SC4674.

Hypochemical protein.

SEQUENCE 249 AA; 28808 MW; 49B1906317386ACC CRC64;

Query Match 35.0%; Score 43; DB 1; Length 249;

Best Local Similarity 31.6%; Pred. No. 20;

Matches 6; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

1 FNRWCLIPACRNKKFC 19

63 FSWHKQMLPRCKRGYVFC 81

SULT 34

22 HUMAN

FOL2_HUMAN STANDARD; PRT; 255 AA.

PI4207;

01-JAN-1990 (Rel. 13, Created)

01-NOV-1995 (Rel. 32, Last sequence update)

10-OCT-2003 (Rel. 42, Last annotation update)

Folate receptor beta precursor (F8-beta) (Folate receptor 2) (Folate

receptor, fetal/placental) (Placental folate-binding protein) (PBP).

FOLR2.

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

[1]

SEQUENCE FROM N.A.

MEDLINE=93188012; PubMed=8445646;

Page S.T., Owen W.C., Price K., Elwood P.C.;

"Expression of the human placental folate receptor transcript is

regulated in human tissues. Organization and full nucleotide sequence

of the gene.";

J. Mol. Biol. 229:1175-1183(1993).

[2]

SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

TISSUE=Placenta;

MEDLINE=90105335; PubMed=2605182;

Ratnam M., Marquardt H., Duhring J.L., Freisheim J.H.;

"Homologous membrane folate binding proteins in human placenta:

cloning and sequence of a cDNA.";

Biochemistry 28:8249-8254(1989).

[3]

SEQUENCE FROM N.A.

TISSUE=Placenta;

MEDLINE=94148914; PubMed=8106441;

Sadasivan E., Cedeno M.M., Rothenberg S.P.;

"Characterization of the gene encoding a folate-binding protein

expressed in human placenta. Identification of promoter activity in a
G-rich SPI site linked with the tandemly repeated GGAAG motif for
the ets encoded GA-binding protein.";

J. Biol. Chem. 269:4725-4735(1994).

[4]

GPI-ANCHOR.

MEDLINE=96062525; PubMed=7578066;

Yan W., Ratnam M.;

"Preferred sites of glycosylphosphatidylinositol modification in

folate receptors and constraints in the primary structure of the

hydrophobic portion of the signal.";

Biochemistry 34:14594-14600(1995).

[5]

PROCESSING.

MEDLINE=98062926; PubMed=9398177;

Wang J., Shen F., Yan W., Wu M., Ratnam M.;

"Proteolysis of the carboxyl-terminal GPI signal independent of GPI

modification as a mechanism for selective protein secretion.";

Biochemistry 36:14583-14592(1997).

CC -!- FUNCTION: Binds to folate and reduced folic acid derivatives and

mediates delivery of 5-methyltetrahydrofolate to the interior of

cells.

CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

CC Also secreted

CC -!- TISSUE SPECIFICITY: FR-BETA LEVELS ARE GREATLY ELEVATED IN A

VARIETY OF MALIGNANT TISSUES OF NONEPITHELIAL ORIGIN COMPARED WITH

NORMAL TISSUES.

CC -!- PTM: Eight disulfide bonds are present (Probable).

CC -!- PTM: N-Glycosylated.

CC -!- SIMILARITY: Belongs to the folate receptor family.

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or send an email to license@isb-sib.ch).

CC -----

EMBL: X69516; CAA49267.1; -

EMBL: J02876; AAA35821.1; -

EMBL: U02714; AAA17370.1; -

EMBL: U02716; AAA17370.1; JOINED.

PIR: AS3315; A33417.

Genew: HGNC:3793; FOLR2.

MIM: 136425; -

GO: GO:0005624; C:membrane fraction; TAS.

GO: GO:0005542; F:folic acid binding; TAS.

GO: GO:0015884; P:folate transport; TAS.

InterPro: IPR004269; Folt.chemrecept.

Pfam: PF03024; Folate rec. 1.

Receptor; Glycoprotein; Signal; Placenta; Folate-binding; Membrane;

GPI-anchor; Multigene family; Lipoprotein.

KW SIGNAL

1 16

CHAIN 17 230

FOLATE RECEPTOR BETA.

REMOVED IN MATURE FORM.

FT PROPEP 231 255

GPI-anchor amidated asparagine.

FT LIPID 230 230

N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 115 115

N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 195 195

T -> S (IN REF. 1).

FT CONFLICT 117 117

H -> L (IN REF. 3).

FT CONFLICT 141 141

S -> R (IN REF. 3).

FT CONFLICT 244 244

SEQUENCE 255 AA; 29293 MW; F0852287A3B81C98 CRC64;

SQ

Query Match 35.0%; Score 43; DB 1; Length 255;

Best Local Similarity 50.0%; Pred. No. 20;

Matches 8; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

QY 1 FNRWCC-LIPACRN 14

78 FNRWCC-LIPACRN 93

Db

SULT 35

15_ARATH
 _CG15_ARATH STANDARD; PRT; 678 AA.
 Q9SL29;
 15-MAR-2004 (Rel. 43, Created)
 15-MAR-2004 (Rel. 43, Last sequence update)
 15-MAR-2004 (Rel. 43, Last annotation update)
 Putative cyclic nucleotide-gated ion channel 15 (cyclic nucleotide-
 and calmodulin-regulated ion channel 15).
 CNGC15 OR AT2G28260 OR T3B23.7.
 Arabidopsis thaliana (Mouse-ear cress).
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 eurosid II; Brassicales; Brassicaceae; Arabidopsids.
 NCBI_TaxID=3702;
 [1]
 SEQUENCE FROM N.A.
 STRAIN=cv. Columbia;
 MEDLINE=20083487; PubMed=10617197;
 Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
 Buell C.R., Ketchum K.A., Lee J.J., Renning C.M., Koo H.L.,
 Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
 Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
 Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
 Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
 Venter J.C.;
 "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 thaliana.";
 Nature 402:761-768(1999).
 [2]
 GENE FAMILY, AND NOMENCLATURE.
 MEDLINE=21392307; PubMed=11500563;
 Maeser P., Thomine S., Schroeder J.I., Ward J.M., Hirschi K., Sze H.,
 Talke I.N., Antmann A., Maathuis F.J.M., Sanders D., Harper J.F.,
 Tchieu J., Gribskov M., Persans M.W., Salt D.E., Kim S.A.,
 Gueriot M.B.;
 "Phylogenetic relationships within cation transporter families of
 Arabidopsis.";
 Plant Physiol. 126:1646-1667(2001).
 -1- FUNCTION: Putative cyclic nucleotide-gated ion channel.
 -1- SUBUNIT: Homotetramer or heterotetramer (Potential).
 -1- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane
 (Potential).
 -1- DOMAIN: The binding of calmodulin to the C-terminus might
 interfere with cyclic nucleotide binding and thus channel
 activation (By similarity).
 -1- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
 (TC 1.A.1.5) family.
 -1- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
 -1- SIMILARITY: Contains 1 IQ domain.

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 or send an email to license@isb-sib.ch).

 EMBL; AC006202; AAD29827.1; -;
 PIR; G84682; G84682.
 InterPro; IPR000595; CNMP binding.
 InterPro; IPR005821; Ion Trans.
 InterPro; IPR000048; IQ_region.
 InterPro; IPR001622; K-channel_pore.
 Pfam; PF00027; CNMP_binding; 1.
 Pfam; PF00520; ion_trans; 1.
 Pfam; PF00612; IQ; 1.
 SMART; SM00100; CNMP; 1.
 PROSITE; PS00888; CNMP_BINDING_1; FALSE_NEG.
 PROSITE; PS00889; CNMP_BINDING_2; FALSE_NEG.
 PROSITE; PS00042; CNMP_BINDING_3; 1.

DR PROSITE; PS00096; IQ; 1.
 KW Hypothetical protein; Ion transport; Ionic channel;
 KW Calmodulin-binding; cAMP-binding; cGMP-binding; Transmembrane;
 KW Multigene family.
 FT DOMAIN 1 81 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 82 102 H1 (POTENTIAL).
 FT DOMAIN 103 115 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 116 136 H2 (POTENTIAL).
 FT DOMAIN 137 170 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 171 191 H3 (POTENTIAL).
 FT DOMAIN 192 203 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 204 224 H4 (POTENTIAL).
 FT DOMAIN 225 245 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 246 266 H5 (POTENTIAL).
 FT DOMAIN 267 364 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 365 385 H6 (POTENTIAL).
 FT DOMAIN 386 678 CYTOPLASMIC (POTENTIAL).
 FT NP_BIND 471 595 CNMP.
 FT BINDING 542 542 CAMP OR CGMP (BY SIMILARITY).
 FT DOMAIN 587 602 CALMODULIN-BINDING (BY SIMILARITY).
 FT DOMAIN 607 638 IQ.
 SQ SEQUENCE 678 AA; 78722 MW; E020D14E44050B64 CRC64;
 Query Match 35.0%; Score 43; DB 1; Length 678;
 Best Local Similarity 46.7%; Pred. No. 51;
 Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
 QY 3 WRCLLPACRRNKK 17
 DB 609 WAACFIQAAMRRHRK 623

Search completed: February 18, 2004, 06:07:09

Job time : 48 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

protein - protein search, using sw model

on: February 18, 2004, 06:03:18 ; Search time 80 Seconds

(without alignments)

74.936 Million cell updates/sec

le: US-09-806-376-1

fect score: 123

uence: 1 FNRCCILPACRRNKKFC 19

ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 1017041 seqs, 315518202 residues

al number of hits satisfying chosen parameters: 1017041

imum DB seq length: 0

imum DB seq length: 2000000000

st-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

abase :

SPTREMBL_25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp Vertebrate:*

14: sp Unclassified:*

15: sp_rvirus:*

16: sp_bacteriaph:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult	No.	Score	Query Match %	Length	DB	ID	Description
1	52	42.3	189	5	Q17888	Q17888 caenorhabdi	
2	51	41.5	328	8	Q8HRP0	Q8hrp0 dipterogium	
3	50.5	41.1	720	5	O01605	O01605 caenorhabdi	
4	49	39.8	82	12	O39626	O39626 cydia pomon	
5	49	39.8	180	2	Q7X4R1	Q7x4r1 streptomyc	
6	49	39.8	188	16	Q8Y300	Q8y300 ralsstonia s	
7	49	39.8	334	16	Q8XZ29	Q8xz29 ralsstonia s	
8	49	39.8	610	4	Q8NRE9	Q8nre9 homo sapien	
9	49	39.8	640	10	Q96397	Q96397 chlamydomon	
10	48.5	39.4	534	11	Q8BLN2	Q8bln2 mus musculu	
11	48	39.0	141	5	Q7YX40	Q7yx40 caenorhabdi	
12	48	39.0	145	16	Q8FK43	Q8fk43 escherichia	
13	48	39.0	338	4	Q9UJ42	Q9uj42 homo sapien	
14	48	39.0	510	4	Q9H846	Q9h846 homo sapien	
15	48	39.0	510	4	Q96GM8	Q96gm8 homo sapien	
16	48	39.0	510	4	Q81WN5	Q81wn5 homo sapien	

Q8K2J3 mus musculu
Q9VPL9 drosophila
Q9NP04 homo sapien
Q9K508 pseudomonas
Q64412 cavia porce
Q28428 gorilla gor
Q86R22 conus geogr
Q854F9 mycobacteri
Q81217 zea mays (m
Q965R6 caenorhabdi
Q69275 equine herp
Q8V723 simian herp
Q75C22 simian herp
Q9LYB6 rattus norv
Q04923 saccharomyc
Q8TN25 methanosarc
Q42558 brachydanio
Q9JMF2 mus musculu
Q9XSH1 sus scrofa
O53533 mycobacteri
Q7VEM6 mycobacteri
Q9H811 homo sapien
Q8MYG9 caenorhabdi
Q38743 antirrhinum
Q13535 homo sapien
Q8WPU0 trypanosoma
O46025 caenorhabdi
Q93291 fugu rubrip
Q8WME4 desmodus ro
Q8WNZ5 moroneus me
Q9WUN4 rattus norv
Q7TXR1 mycobacteri
Q8XM87 clostridium
Q91CZ3 tt virus. O

ALIGNMENTS

RESULT 1

Q17888 PRELIMINARY; PRT; 189 AA.
AC Q17888;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN Cl0A4.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Bristol N2;
RA None;
RA MEDLINE=99069613; PubMed=9851916;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Bristol N2;
RA Pauley A.;
RT "The sequence of C. elegans cosmid Cl0A4.";
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U23454; AAC46520.1; -.

PIR; T15479; T15479.
 WormPep: C10A4.6; CE02474.
 Hypothetical protein.
 SEQUENCE 169 AA; 22250 MW; 218F93C56EC773CE CRC64;
 Query Match 42.3%; Score 52; DB 5; Length 189;
 Best Local Similarity 44.4%; Pred. No. 1.6; Indels 10; Gaps 1;
 Matches 12; Conservative 1; Mismatches 4;
 1 FNWRCCCLIPA-----CRNHKK 17
 |||||
 144 FNRCCQCATKMKLMNQICRRNGK 170
 |||||
 QSHRPO PRELIMINARY; PRT; 328 AA.
 QSHRPO;
 01-MAR-2003 (TrEMBLrel. 23, Created)
 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 NADH dehydrogenase subunit F (fragment).
 NDHF.
 Dipterygium glaucum.
 Chloroplast.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 eurosids II; Brassicales; Brassicaceae; Dipterygium.
 NCBI_TaxID=202664;
 [1]
 SEQUENCE FROM N.A.
 Hall J.C., Sytsma K.J., Iltis H.H.;
 "Phylogeny of Caparraceae and Brassicaceae based on chloroplast
 sequence data.";
 Am. J. Bot. 89:1826-1842(2002).
 EMBL; AY122392; AA82796.1; -.
 GO; GO:0009507; C:Chloroplast; IEA.
 GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
 GO; GO:0006120; P:mitochondrial electron transport, NADH to u. .; IEA.
 InterPro; IPR001750; Oxidored q1.
 InterPro; IPR002128; Oxidored q1.
 Pfam; PF00361; oxidored q1; 1-1_C.
 Pfam; PF01010; oxidored q1_C; 1.
 Chloroplast.
 NON_TER 1
 NON_TER 328
 SEQUENCE 328 AA; 37788 MW; 64E91EC91874E793 CRC64;
 Query Match 41.5%; Score 51; DB 8; Length 328;
 Best Local Similarity 50.0%; Pred. No. 3.7; Indels 4; Gaps 1;
 Matches 11; Conservative 1; Mismatches 6;
 2 NWRCCCLIPACRENHK-----FC 19
 |||||
 126 NNFCLVPLLRNHKKVSCFC 147
 |||||
 Q01605 PRELIMINARY; PRT; 720 AA.
 Q01605;
 01-JUL-1997 (TrEMBLrel. 04, Created)
 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 Hypothetical protein.
 Caenorhabditis elegans.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 Rhabditidae; Peloderinae; Caenorhabditis.
 NCBI_TaxID=6239;
 [1]
 SEQUENCE FROM N.A.
 STRAIN=Bristol N2;
 RX

RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Bristol N2;
 RC STRAIN=Bristol N2;
 RA Greco T., Hawkins M.;
 RT "The sequence of C. elegans cosmid T10E9.";
 RL submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Bristol N2;
 RC Waterston R.;
 RA "Direct Submission.";
 RL submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U97403; AA852470.1; -.
 DR PIR; T25883; T25883.
 DR WormPep; T10E9.2; CE13545.
 KW Hypothetical protein.
 SQ SEQUENCE 720 AA; 83989 MW; 9A6D9E8B3E55E05 CRC64;
 Query Match 41.1%; Score 50.5; DB 5; Length 720;
 Best Local Similarity 60.0%; Pred. No. 8.7;
 Matches 9; Conservative 0; Mismatches 3; Indels 3; Gaps 1;
 QY 1 FNRCCCLIPACRENH 15
 |||||
 DB 347 FNRCCCL---CPRAH 358
 |||||
 RESULT 4
 O39626 PRELIMINARY; PRT; 82 AA.
 ID O39626
 AC O39626;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE ORF353a (ORF42 similar to XcGV ORF36).
 GN ORF42.
 OS Cydia pomonella granulosis virus (CpGV) (Cydia pomonella
 granulovirus).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
 OX NCBI_TaxID=28289;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jehle J.A., van der Linden I.F.A., Vlask J.M.;
 RT "Identification and sequence analysis of the integration site of
 RT transposon TcP3.2 in the genome of Cydia pomonella granulovirus.";
 RL Virus Res. 0:0-0(1997).
 [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Mexican 1;
 RC STRAIN=Mexican 1;
 RX MEDLINE=93188168; PubMed=8445726;
 RA Crook N.E., Clem R.J., Miller L.K.;
 RT "An apoptosis-inhibiting baculovirus gene with a zinc finger-like
 RT motif.";
 RL J. Virol. 67:2168-2174 (1993).
 [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Mexican 1;
 RC STRAIN=Mexican 1;
 RX MEDLINE=96207404; PubMed=8615018;
 RA Theilmann D.A., Chantler J.K., Stewart S., Flippen H.T., Vlask J.M.,
 RA Crook N.E.;
 RT "Characterization of a highly conserved baculovirus structural protein
 RT that is specific for occlusion-derived virions.";
 RL Virology 218:148-158(1996).
 [4]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Mexican 1;
 RC STRAIN=Mexican 1;
 RX MEDLINE=97380577; PubMed=9237352;
 RA Kang W., Crook N.E., Winstanley D., O'Reilly D.R.;

SEQUENCE 334 AA; 35204 MW; 0FC0176E32E8F3BA2 CRC64;
Query Match 39.8%; Score 49; DB 16; Length 334;
Best Local Similarity 41.2%; Pred. No. 7.8;
Matches 7; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
3 WRCCLIPACRRNHKKFC 19
89 WSCGTCTPCRRDQENLC 105
SULT 8
Q9NRE9 PRELIMINARY; PRT; 610 AA.
Q9NRE9; 01-OCT-2000 (TRENBLrel. 15, Created)
01-OCT-2000 (TRENBLrel. 15, Last sequence update)
01-JUN-2003 (TRENBLrel. 24, Last annotation update)
Cone photoreceptor cGMP-gated cation channel beta-subunit.
CNGB3.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=Retina;
MEDLINE=20347712; PubMed=10888875;
Sundin O.H., Yang J.-M., Li Y., Zhu D., Hurd J.N., Mitchell T.H.,
Silva E.D., Maumenee I.H.;
"Genetic basis of total colourblindness among the Pingelapese
islanders.";
Nat. Genet. 25:289-293(2000).
EMBL; AF228520; RA080179.1; -;
GO; GO:0007601; P:vision; TAS.
InterPro; IPR000595; CNMP binding.
InterPro; IPR005821; Ion trans.
InterPro; IPR001622; K-channel_pore.
Pfam; PF00027; CNMP binding; 1.
Pfam; PF00520; ion trans; 1.
SMART; SM00100; CNMP; 1.
PROSITE; PS00888; CNMP_BINDING_1; 1.
PROSITE; PS50042; CNMP_BINDING_3; 1.
Ionic channel; Receptor; Transmembrane.
SEQUENCE 610 AA; 70039 MW; 843B01F12643B73A CRC64;
Query Match 39.8%; Score 49; DB 4; Length 610;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
1 FNRWCCCLIP 9
35 YNWNCCFIP 43
SULT 9
Q96397 PRELIMINARY; PRT; 640 AA.
Q96397; O04833; O04733;
01-FEB-1997 (TRENBLrel. 02, Created)
01-FEB-1997 (TRENBLrel. 02, Last sequence update)
01-JUN-2003 (TRENBLrel. 24, Last annotation update)
LKG5.
LKG5.
Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Voivocales;
Chlamydomonadaceae; Chlamydomonas.
NCBI_TaxID=3055;
[1]
SEQUENCE FROM N.A.
Gloeckner G., Beck C.F.;
Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
[2]

RP SEQUENCE FROM N.A.
RA Gloeckner G., Beck C.F.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U73817; AB17561.1; -;
DR EMBL; U73818; AB39840.1; -;
DR PIR; T08179; T08179.
DR InterPro; IPR001007; VWF_C.
DR PROSITE; PS01208; VWF_C_1;
SQ SEQUENCE 640 AA; 67298 MW; 764BEE7ADC32FC99 CRC64;
Query Match 39.8%; Score 49; DB 10; Length 640;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2 NWRCCCLIPAC 11
DB 586 NWCCCLPGC 595
RESULT 10
Q8BLN2 PRELIMINARY; PRT; 534 AA.
ID Q8BLN2;
AC Q8BLN2;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Weakly similar to kinesin heavy chain-like protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=22354683; PubMed=12456851;
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK044049; BAC31752.1; -;
FT NON_TER
SQ SEQUENCE 534 AA; 58612 MW; 71AD5390D8D7322F CRC64;
Query Match 39.4%; Score 48.5; DB 11; Length 534;
Best Local Similarity 40.9%; Pred. No. 14;
Matches 9; Conservative 3; Mismatches 3; Indels 7; Gaps 1;
QY 2 NW-----RCCLIPACRRNHK 16
DB 512 NWKLSSTLNRCCLVYHRPHHE 533
RESULT 11
Q7YX40 PRELIMINARY; PRT; 141 AA.
ID Q7YX40;
AC Q7YX40;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein F36G3.3.
GN F36G3.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OC NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology.";


```

Science 282:2012-2018(1998).
[2]
SEQUENCE FROM N.A.
STRAIN=Bristol N2;
White S.; (DEC-1994) to the EMBL/GenBank/DBJ databases.
EMBL; 247069; CAB17781.1; -.
Hypothetical protein.
SEQUENCE 141 AA; 15967 MW; 24E55561B1EBD95B CRC64;

Query Match 39.0%; Score 48; DB 5; Length 141;
Best Local Similarity 50.0%; Pred. No. 5.4; Indels 0; Gaps 0;
atches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

3 WRCCFLPACRRNHK 16
|||||:|:|:|
109 WCCCFLPCLRSCK 122

ULT 12
K43 Q8FK43 PRELIMINARY; PRT; 145 AA.
Q8FK43;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein ypci.
YBCI OR C0643.
Escherichia coli O6.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
[1]
SEQUENCE FROM N.A.
STRAIN=O6:H1 / CFT073 / ATCC 700928;
MEDLINE=22388234; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
EMBL; AE016757; AA079120.1; -.
InterPro; IPR007404; DUF457.
Pfam; PF04307; DUF457; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 145 AA; 16877 MW; 1004B10029242686 CRC64;

Query Match 39.0%; Score 48; DB 16; Length 145;
Best Local Similarity 58.3%; Pred. No. 5.5;
atches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

2 NWRCCLPACRR 13
|||||:|:|:|
5 SWRCCLPMTYR 16

ULT 13
J042 Q9UJ42 PRELIMINARY; PRT; 338 AA.
Q9UJ42;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Putative G-protein coupled receptor.
GPCR150 OR GPCR.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=Pancreas;
Conklin D., Yee D., Engelbrecht J., Vissing H.;
"Mining of Assembled EST Data in Protein Super families: Application
to the G-Protein-Coupled Receptors.";
Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Cervix;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RP Takeda S., Kadowaki S., Haga T., Takasu H., Mitaku S.;
RT "Identification of G protein-coupled receptor genes from the human
genome sequence.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ249248; CAB55314.1; -.
DR EMBL; BC000181; AA00181.1; -.
DR EMBL; AB083583; BAB89296.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR Rhodpsn.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW RECEPTOR.
SQ SEQUENCE 338 AA; 39786 MW; 50B38F90E0311175 CRC64;

Query Match 39.0%; Score 48; DB 4; Length 338;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NWRCCCLIP 9
|||||:|:|:|
DB 313 NWRCCCFIP 320

RESULT 14
Q9H846 PRELIMINARY; PRT; 510 AA.
AC Q9H846
AC Q9H846; 2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ13949.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura K., Nagahari K., Masuno Y.,
RA Nimomiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK024011; BAB14774.1; -.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR006941; CAP1.
DR InterPro; IPR000571; Znf_CCCH.
DR Pfam; PF04857; CAP1; 1.
DR Pfam; PF00642; zf-CCCH; 1.
KW Hypothetical protein.
SQ SEQUENCE 510 AA; 56566 MW; FFA612937B012252 CRC64;

Query Match 39.0%; Score 48; DB 4; Length 510;
Best Local Similarity 57.1%; Pred. No. 16;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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ULT 15
GNM8 2 NWRCLIPACRRNH 15
:|||||
282 DYRCCLPPATHRPH 295

Q96GM8 PRELIMINARY; PRT; 510 AA.
Q96GM8; 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISUB=Uterus;
Strausberg R.;
Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
EMBL; BC009364; AA09364.1; -
Genew; HGNC:15954; TOE1.
GO; GO:0003676; P:nucleic acid binding; IEA.
InterPro; IPR006941; CAP1.
InterPro; IPR000571; Znf_CCHH.
Pfam; PF04857; CAF1; 1.
Pfam; PF00642; zf-CCCH; 1.
Hypothetical protein.
SEQUENCE 510 AA; 56547 MW; 584616F50E12929 CRC64;

Query Match 39.0%; Score 48; DB 4; Length 510;
Best Local Similarity 57.1%; Pred. No. 16;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

2 NWRCLIPACRRNH 15
:|||||
282 DYRCCLPPATHRPH 295

ULT 16
GNM5 2 NWRCLIPACRRNH 15
:|||||
Q8IWN5 PRELIMINARY; PRT; 510 AA.
Q8IWN5; 01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Target of Egri protein.
TOE1.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
de Belle I., Wu J.-X., Sperandio S., Mercola D., Adamson E.D.;
"In vivo cloning and characterization of a new growth suppressor
protein TOE1 as a direct target of Egri.";
Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
EMBL; AY169960; AAN75441.1; -
GO; GO:0003676; P:nucleic acid binding; IEA.
InterPro; IPR006941; CAP1.
InterPro; IPR000571; Znf_CCHH.
Pfam; PF04857; CAF1; 1.
Pfam; PF00642; zf-CCCH; 1.
SEQUENCE 510 AA; 56489 MW; E3D616F59C2E2A85 CRC64;

Query Match 39.0%; Score 48; DB 4; Length 510;
Best Local Similarity 57.1%; Pred. No. 16;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

2 NWRCLIPACRRNH 15

Db 282 DYRCCLPPATHRPH 295
:|||||

RESULT 17
Q8K2J3 PRELIMINARY; PRT; 636 AA.
AC Q8K2J3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC031207; AAH31207.1; -
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 636 AA; 72242 MW; 3C5C72EACACEFE055 CRC64;

Query Match 39.0%; Score 48; DB 11; Length 636;
Best Local Similarity 52.9%; Pred. No. 20;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 FNWRCLIPACRRNHK 17
:|||||
DB 496 FDMKCLPPAGVENYK 512

RESULT 18
Q9VPL9 PRELIMINARY; PRT; 5322 AA.
AC Q9VPL9; Q9NI64;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CG3696 protein (KISMET-L long isoform).
GN KIS OR CG3660 OR CG3696 OR CG18326.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Ephydroidea; Drosophilidae; Diptera; Brachycera; Muscomorpha.

OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers J.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Niklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.N., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hosain D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J., Williams S.M., Woodgate T., Worley K.C., Wu D., Yang S., Yao O.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 "The genome sequence of *Drosophila melanogaster*";
 Science 287:2185-2195(2000).
 [2]
 SEQUENCE FROM N.A.
 Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A., Evans C.A., Gocayne J.D., Ananides P.G., Brandon R.C., Rogers Y., Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A., Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M., Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D., Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A., Gonzalez M., Houch J., Hoskins R.A., Hostin D., Howland T.J., Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J., Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 "Sequencing of *Drosophila melanogaster* genome";
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [3]
 SEQUENCE FROM N.A.
 Misra S., Creeby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D., Tupy J.L., Bergman C., Bertram B., Carlson J.W., Celniker S.E., Clump M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak P., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 "Annotation of *Drosophila melanogaster* genome";
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [4]
 SEQUENCE FROM N.A.
 Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [5]
 SEQUENCE FROM N.A.
 FlyBase;
 Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 [6]
 SEQUENCE FROM N.A.
 Therrien M., Morrison D.K., Wong A.M., Rubin G.M.;
 "A Genetic Screen for Modifiers of a KR-dependent Rough Eye Phenotype in *Drosophila*";
 Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 EMBL; AF003590; AAF51527.3; -
 EMBL; AF215703; AAF43004.1; -
 HSPB; P23197; IAP0.
 FlyBase; FBgn0001309; kis.
 GO; GO:0000785; C:nucleus; IEA.
 GO; GO:0005634; C:nucleus; IEA.
 GO; GO:0005524; F:ATP binding; IEA.
 GO; GO:0008026; F:ATP dependent helicase activity; IEA.
 GO; GO:0003682; F:chromatin binding; IEA.
 GO; GO:0016787; F:hydrolase activity; IEA.
 GO; GO:0006333; P:chromatin assembly/disassembly; IEA.
 InterPro; IPR000953; Chromo.
 InterPro; IPR001410; DEAD.
 InterPro; IPR001650; Helicase_C.

DR InterPro; IPR000330; SNF2_N.
 DR Pfam; PF00385; Chromo; 1.
 DR Pfam; PF00271; helicase C; 1.
 DR Pfam; PF00176; SNF2 N; 1.
 DR SMART; SM00298; CHROMO; 2.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELIC; 1.
 DR PROSITE; PSS0013; CHROMO.2; 1.
 KW ATP-binding; Helicase; Hydrolase.
 SQ SEQUENCE 5322 AA; 573615 MW; C9608375FA71C211 CRC64;
 Query Match 39.0%; Score 48; DB 5; Length 5322;
 Best Local Similarity 42.1%; Pred. No. 1.2e+02;
 Matches 8; Conservative 2; Mismatches 9; Indels 0; Gaps 0;
 Qy 1 FNRCCILIPACRRNHKKFC 19
 Db 2158 FNRWLCVIDEHLKRNRC 2176
 RESULT 19
 Q9NP04 PRELIMINARY; PRT; 105 AA.
 ID Q9NP04
 AC Q9NP04
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Folate receptor alpha isoform (Fragment).
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94339186; PubMed=8061055;
 RA Prasad P.D., Ramamoorthy S., Moe A.J., Smith C.H., Leibach F.H., Ganapathy V.;
 RT "Selective expression of the high-affinity isoform of the folate receptor (FR-alpha) in the human placental syncytiotrophoblast and choriocarcinoma cells.";
 RL Biochim. Biophys. Acta 1223:71-75(1994).
 DR EMBL; S73490; AAB31700.1; -
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR004269; Folt_chemrecept.
 DR Pfam; PF03024; Folate_rec; 1.
 KW Receptor.
 FT NON TER 105 105
 SQ SEQUENCE 105 AA; 12225 MW; B30DE586EFB2CE9 CRC64;
 Query Match 38.2%; Score 47; DB 4; Length 105;
 Best Local Similarity 50.0%; Pred. No. 6;
 Matches 8; Conservative 3; Mismatches 3; Indels 2; Gaps 1;
 Qy 1 FNRCC--LIPACRRN 14
 Db 84 FNRWLCVIDEHLKRNRC 99
 RESULT 20
 Q9K508 PRELIMINARY; PRT; 283 AA.
 ID Q9K508
 AC Q9K508;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Pseudomonas syringae (pv. pisci).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=59510;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=race 2;

Arnold D.L., Jackson R.W., Vivian A.;
"Evidence for the mobility of an avirulence gene, *avrPpiA1*, between
the chromosome and plasmids of races of *Pseudomonas syringae* pv.
plasi.";

Mol. Plant Pathol. 1:195-199(2000).

EMBL; AJ251482; CAB96973.1; -

InterPro; IPR003738; DUF159.

Pfam; PF02586; DUF159; 1.

Hypothetical protein.

SEQUENCE 283 AA; 31984 MW; 6461D7CF59A5ADDE CRC64;

Query Match 38.2%; Score 47; DB 2; Length 283;

Best Local Similarity 34.8%; Pred. No. 14;

Matches 8; Conservative 6; Mismatches 3; Indels 6; Gaps 1;

1 FNRCC-----LIPACRNHKK 17

18 FDWDCCHQLTLQACQSVRQ 40

SULT 21

1412

Q64412 PRELIMINARY; PRT; 46 AA.

Q64412;

01-NOV-1996 (TrEMBLrel. 01, Created)

01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Protamine 1 (Sperm protamines P1) (Fragment).

PM1.

Cavia porcellus (Guinea pig).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.

NCBI_TaxID=10141;

[1]

SEQUENCE FROM N.A.

Queralt R., Adroer R., Oliva R.;

"Protamine 1 cDNA and genomic sequence from the guinea pig (Cavia

porcellus) reveals marked differences to mouse and rat protamines.";

Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.

-!- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF

SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT

SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX (BY

SIMILARITY).

-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE PROTAMINE P1 FAMILY.

EMBL; M83895; AA58348.1; -

GO; GO:0005694; C:chromosome; IEA.

GO; GO:0000786; C:nucleosome; IEA.

GO; GO:0003634; C:nucleus; IEA.

GO; GO:0003677; F:DNA binding; IEA.

GO; GO:0007001; P:chromosome organization and biogenesis (gen. . .; IEA.

GO; GO:0007076; P:mitotic chromosome condensation; IEA.

GO; GO:0007283; P:spermatogenesis; IEA.

InterPro; IPR000221; Protamine P1.

Pfam; PF00260; Protamine P1; 1.

PROSITE; PS00048; PROTAMINE_P1; 1.

Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein;

Nucleosome core; Spermatogenesis.

NON_TER 46 46

SEQUENCE 46 AA; 6218 MW; BB82967CC408463D CRC64;

Query Match 37.8%; Score 46.5; DB 11; Length 46;

Best Local Similarity 42.1%; Pred. No. 3.6;

Matches 8; Conservative 4; Mismatches 4; Indels 3; Gaps 1;

3 WRCCLIPIA---CRRNHKKF 18

4 YRCRSPSRRCRRRRRRF 22

SULT 22

3428

Q28428 PRELIMINARY; PRT; 24 AA.

Q28428;

01-NOV-1996 (TrEMBLrel. 01, Created)

01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

Relaxin (Fragment).

GN RLK.

OS Gorilla gorilla (gorilla).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.

NCBI_TaxID=9593;

[1]

SEQUENCE FROM N.A.

SRRAIN-RG YK; Fu P., Tresegar G.G.W.;

Evans B.B.A., "Characterisation of primate relaxin genes.";

J. Mol. Endocrinol. 0:0-0(1993).

-!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

EMBL; Z27226; CAA81740.1; -

PIR; S42778; S42778.

HSP; P04090; 6RLX.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005179; P:hormone activity; IEA.

GO; GO:0007582; P:physiological processes; IEA.

InterPro; IPR004825; Ins/IGF/relax.

Pfam; PF00049; Insulin; 1.

PROSITE; PS00262; INSULIN; 1.

NON_TER 1

SEQUENCE 24 AA; 2766 MW; 668743C18CBF5927 CRC64;

Query Match 37.4%; Score 46; DB 6; Length 24;

Best Local Similarity 43.8%; Pred. No. 2.4;

Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 4 RCCLIPACRNHKKFC 19

DB 9 KCCLIGCTKRSKLYC 24

RESULT 23

Q86RB2

ID Q86RB2 PRELIMINARY; PRT; 40 AA.

AC Q86RB2;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Alpha-conotoxin G1C precursor (Fragment).

OS Conus geographus (Geography cone).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;

OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;

OC Neogastropoda; Conoidea; Conidae; Conus.

NCBI_TaxID=6491;

[1]

SEQUENCE FROM N.A.

RE MEDLINE=2206623; PubMed=12114524;

RA McIntosh J.M., Dowell C., Watkins M., Garrett J.B., Yoshikami D.,

Olivera B.M.;

"Alpha-Conotoxin G1C from Conus geographus, a Novel Peptide Antagonist

of Nicotinic Acetylcholine Receptors.";

J. Biol. Chem. 277:33610-33615(2002).

EMBL; AF526267; AA033169.1; -

NON_TER 1

CHAIN 21 36 ALPHA-CONOTOXIN G1C.

SEQUENCE 40 AA; 4246 MW; 1414332030CC89D CRC64;

Query Match 37.4%; Score 46; DB 5; Length 40;

Best Local Similarity 46.7%; Pred. No. 3.8;

Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRNHKKFC 19

DB 22 CSHFPACGNQHIC 36

ULT 24
479

Q854F9 PRELIMINARY; PRT; 125 AA.
Q854F9; 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Gp108.
108.
Mycobacteriophage Omega.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBI_TaxID=205879;
[1]
SEQUENCE FROM N.A.
MEDLINE=22592660; PubMed=12705866;
Pedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C.,
Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Panunzio N.R.,
Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S.,
Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,
Hatfull G.F.,
"Origins of highly mosaic mycobacteriophage genomes.";
Cell 113:171-182(2003).
EMBL; AY129338; AA12749.1; -
SEQUENCE 125 AA; 14846 MW; C08BBC3D26687306 CRC64;

Query Match 37.4%; Score 46; DB 9; Length 125;
Best Local Similarity 44.4%; Pred. No. 10;
Matches 8; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

4 RCCLIPACRRNH--KKFC 19
2 RTCTIPGCEKHARGFC 19

ULT 25
217

O81217 PRELIMINARY; PRT; 174 AA.
O81217; 01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Trypsin inhibitor.
Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
NCBI_TaxID=4577;
[1]
SEQUENCE FROM N.A.
STRAIN=TX5855; TISSUE=Root tip;
Finkelstein D.B., Drew M.C., Jordan W.J., Wing R.A., Mullet J.E.,
Morgan P.W.,
Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
EMBL; AF057184; AAC24570.1; -
PIR; T01649; T01649.
HSP; F01064; IPI2.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0004867; F:serine protease inhibitor activity; IEA.
InterPro; IPR000877; Bowman-Birk leg.
Pfam; PF00228; Bowman-Birk leg; 3.
ProDom; PD002168; Bowman-Birk leg; 2.
SMART; SM00269; Bows; 2.
SEQUENCE 174 AA; 19066 MW; 8F14EF058F817046 CRC64;

Query Match 37.4%; Score 46; DB 10; Length 174;
Best Local Similarity 35.3%; Pred. No. 13;
Matches 6; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

3 WRCCLIACRRNHKKFC 19
113 WDCCDFAVCTRDYIPYC 129

RESULT 26

Q96SR6 PRELIMINARY; PRT; 314 AA.
AC Q96SR6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN Y37E10B.2
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
CX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Harmon G., Wohldmann P.;
RT "The sequence of C. elegans cosmid Y97E10B.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Waterston R.;
RT "Direct Submission.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC024881; AAK71412.2; -
DR WormPep; Y97E10B.2; CE30329.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR Rhodopsn.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 314 AA; 36044 MW; 158694F853AASCA3 CRC64;

Query Match 37.4%; Score 46; DB 5; Length 314;
Best Local Similarity 53.3%; Pred. No. 22;
Matches 8; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

Qy 2 NWFCCLIACRRNHK 16
Db 277 SWSG--IPCCRLHK 289

RESULT 27

Q69275 PRELIMINARY; PRT; 363 AA.
AC Q69275;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE US1 protein.
GN US1.
OS Equine herpesvirus 4.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
CX NCBI_TaxID=10331;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=405/76;
RX MEDLINE=9311267; PubMed=8380320;
RA Nagesha H.S., Studdert M.J., Crabb B.S.;
RT "Analysis of the nucleotide sequence of five genes at the left end of
the unique short region of the equine herpesvirus 4 genome.";

Arch. Virol. 128:143-154(1993).
 EMBL; M89634; AAA46100.1; --
 PIR; A48338; A48338.
 SEQUENCE 363 AA; 41068 MW; 3C4096F474C32ED6 CRC64;

Query Match 37.4%; Score 46; DB 12; Length 363;
 Best Local Similarity 87.5%; Pred. No. 25;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

4 RCCLIPAC 11

|||||

284 RCCLTPAC 291

MULT 28

723

Q8V723 PRELIMINARY; PRT; 401 AA.

Q8V723; 01-MAR-2002 (TrEMBLrel. 20, Created)

01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

Glycoprotein gi.

US7.

Simian herpes B virus (Cercopithecoid herpesvirus 1) (Shbv).

Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

Alphaherpesvirinae; Simplexvirus.

NCBI_TaxID=10325;

[1]

SEQUENCE FROM N.A.

STRAIN=E2490;

MEDLINE=21635528; PubMed=11773425;

Ohnawa K., Black D.H., Sato H., Eberle R.;

"Sequence and Genetic Arrangement of the Us Region of the Monkey B

Virus (Cercopithecine herpesvirus 1) Genome and Comparison with the Us

Region of Other Primate Herpesviruses.";

J. Virol. 76:1516-1520(2002).

EMBL; AB074432; BAB83754.1; --

InterPro; IPR002874; Herpes_gi.

Pfam; PF01688; Herpes_gi.1.

SEQUENCE 401 AA; 41980 MW; B4D41D21BA3D3AC3 CRC64;

Query Match 37.4%; Score 46; DB 12; Length 401;

Best Local Similarity 53.8%; Pred. No. 27;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

5 CCLIPACRRNKKK 17

|||||

308 CCLARRCRRRHR 320

SULT 29

75C2

Q7T5C2 PRELIMINARY; PRT; 401 AA.

Q7T5C2; 01-OCT-2003 (TrEMBLrel. 25, Created)

01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Virion glycoprotein 1.

US7.

Simian herpes B virus (Cercopithecoid herpesvirus 1) (Shbv).

Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

Alphaherpesvirinae; Simplexvirus.

NCBI_TaxID=10325;

[1]

SEQUENCE FROM N.A.

STRAIN=E2490;

MEDLINE=22628476; PubMed=12743273;

Pereiygina L., Zhu L., Zerkhulen H., Mills R., Borodovsky M.,

Hilliard J.K.;

"Complete Sequence and Comparative Analysis of the Genome of Herpes B

Virus (Cercopithecine Herpesvirus 1) from a Rhesus Monkey.";

J. Virol. 77:6167-6177(2003).

EMBL; AF533768; AAP41484.1; --

SQ SEQUENCE 401 AA; 42025 MW; 5DAFECDB58D357C CRC64;
 Query Match 37.4%; Score 46; DB 12; Length 401;
 Best Local Similarity 53.8%; Pred. No. 27;
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 5 CCLIPACRRNKKK 17

|||||

Db 308 CCLARRCRRRHR 320

RESULT 30

Q91YB6

ID Q91YB6 PRELIMINARY; PRT; 1236 AA.

AC Q91YB6;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DB Complement inhibitory factor H.

GN FH.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

SEQUENCE FROM N.A.

RP STRAIN=Sprague-Dawley; TISSUE=Liver;

RA Denberg R., Goetze O., Schlaf G.;

RT "Rat complement factor H: molecular cloning, sequencing and expression

in tissues and isolated cells.";

RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ320522; CAC67513.1; --

DR InterPro; IPR000436; Sushi_SCR_CCP.

DR InterPro; IPR007087; Znf_C2H2.

DR Pfam; PF00084; sushi; 20.

DR SMART; SMO0032; CCP; 20.

DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.

SQ SEQUENCE 1236 AA; 140343 MW; 1AC89FFA28232BBF CRC64;

Query Match 37.4%; Score 46; DB 11; Length 1236;

Best Local Similarity 63.6%; Pred. No. 72;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PACRRNKKFC 19

|||||

Db 800 FNCTRNEKFC 910

RESULT 31

Q04923

ID Q04923 PRELIMINARY; PRT; 97 AA.

AC Q04923;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein.

GN YDR220C.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

OX NCBI_TaxID=4932;

RN [1]

SEQUENCE FROM N.A.

RC STRAIN=AB972;

RA Murphy L., Harris D.;

RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.

RN [2]

SEQUENCE FROM N.A.

RP STRAIN=AB972;

RA Barrell B., Rajandream M.A.;

RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.

RN [3]

SEQUENCE FROM N.A.

STRAIN=AB972; MEDLINE=97039860; PubMed=8885406; de Virgilio C., DeMarini D.J., Pringle J.R., "SPX28, a sixth member of the septin gene family in Saccharomyces cerevisiae that is expressed specifically in sporulating cells."; Microbiology 142:2897-2905(1996). EMBL; Z48612; CAAB8500.1; - PIR; S59427; S59427. SGD; S0002628; YDR220C. Hypothetical protein. SEQUENCE 97 AA; 11171 MW; 3AFA5626B0A99BE8 CRC64; Query Match 37.0%; Score 45.5; DB 3; Length 97; Best Local Similarity 42.1%; Pred. No. 9.7; Mismatches 5; Gaps 2; Matches 8; Conservative 5; Indels 1; Gaps 5;	1 FNRWCLLPACRRNHKKFC 19 :: :: :: :: 53 YSW-CCLL----RNYKRLC 66	ULT 32 N25 Q8TN25; PRELIMINARY; PRT; 350 AA. 01-JUN-2002 (TRENBLrel. 21, Created) 01-JUN-2002 (TRENBLrel. 21, Last sequence update) 01-MAR-2003 (TRENBLrel. 23, Last annotation update) Hypothetical protein MA2468. MA2468. Methanosarcina acetivorans. Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis; Methanosarcinales; Methanosarcinaceae; Methanosarcina. NCBI_TaxID=2214; [1] SEQUENCE FROM N.A. STRAIN=CZA / ATCC 35395 / DSM 2834; MEDLINE=21929760; PubMed=11932238; Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P., FitzHugh W., Calvo J., Engels R., Smirnov S., Atnoor D., Brown A., Allen N., Naylor J., Stange-Thomann N., Dearellano K., Johnson R., Linton L., McSwan P., McKernan K., Talanas J., Tirrell A., Ye W., Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M., Hedderich R., Ingram-Smith C., Kuettnner H.C., Krzycki J.A., Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K., Springer T.A., Unayam L.A., White O., White R.H., de Macario E.C., Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I., Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E., Metcalfe W.W., Birren B.; "The genome of Methanosarcina acetivorans reveals extensive metabolic and physiological diversity."; Genome Res. 12:532-542(2002). EMBL; AB010940; AAM05854.1; - InterPro; IPR003455; DUF142. Pfam; PF02409; Ont N; 1 Hypothetical protein; Complete proteome. SEQUENCE 350 AA; 39330 MW; BAAEDB42978FD10 CRC64; Query Match 37.0%; Score 45.5; DB 17; Length 350; Best Local Similarity 72.7%; Pred. No. 29; Mismatches 2; Indels 1; Gaps 1; Matches 8; Conservative 0; Indels 1; Gaps 1;	3 WPCCLL-PACR 12 :: :: :: 34 WACCLCPACR 44	ULT 33 558 Q42558 PRELIMINARY; PRT; 28 AA. O42558; 01-JAN-1998 (TRENBLrel. 05, Created) 01-JAN-1998 (TRENBLrel. 05, Last sequence update)	01-OCT-2003 (TRENBLrel. 25, Last annotation update) TRA (Fragment). THRAL. OS Brachydanio rerio (Zebrafish) (Danio rerio). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes; OC Cyprinidae; Danio. OX NCBI_TaxID=7955; [1] SEQUENCE FROM N.A. RX MEDLINE=97338099; PubMed=9192646; RA Escrivá H., Safi R., Hanni C., Langlois M.C., Saumitou-Laprade P., Stehelin D., Capron A., Pierce R., Laudet V.; "Ligand binding was acquired during evolution of nuclear receptors."; Proc. Natl. Acad. Sci. U.S.A. 94:6803-6808(1997). RL - - SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY). CC - - SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY. DR EMBL; U93485; AAB68762.1; - DR ZFIN; ZDB-GENE-990415-266; thral. DR GO; GO:0005634; C:nucleus; IEA. DR GO; GO:0004872; P:receptor activity; IEA. DR GO; GO:0003700; F:transcription factor activity; IEA. DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA. DR GO; GO:0006355; P:transcription; IEA. DR InterPro; IPR008946; Str ncl receptor. DR Pfam; PF00105; zf-C4; 1. DR ProDom; PD000035; Znf_C4steroid; 1. KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription; KW Transcription regulation; Zinc; Zinc-finger. FT NON_TER 1 28 FT NON_TER 28 28 SQ SEQUENCE 28 AA; 3325 MW; F457DD9256A06906 CRC64; Query Match 36.6%; Score 45; DB 13; Length 28; Best Local Similarity 46.7%; Pred. No. 4; Mismatches 2; Indels 0; Gaps 0; Matches 7; Conservative 2; Indels 0; Gaps 0;	5 CCLIPACRRNHKKFC 19 :: :: :: 13 CCIDKXITRNHCQHC 27	Db RESULT 34 Q9JMF2 ID Q9JMF2 PRELIMINARY; PRT; 237 AA. AC Q9JMF2; DT 01-OCT-2000 (TRENBLrel. 15, Created) DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update) DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update) DE Unknown protein (Fragment). GN 3322402L07RIK. OS Mus musculus (Mouse). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. OX NCBI_TaxID=10090; [1] SEQUENCE FROM N.A. RP TISSUE=Brain; RX MEDLINE=20145471; PubMed=10679242; RA Inoue S., Sano H., Ohta M.; RT "Growth suppression of Escherichia coli by induction of expression of mammalian genes with transmembrane or Arpase domains."; RL Biochem. Biophys. Res. Commun. 268:553-561(2000). DR EMBL; AB030195; BAA92758.1; - DR MGD; MGI:1921273; 3322402L07RIK. FT NON_TER 1 1 FT NON_TER 1 1 SQ SEQUENCE 237 AA; 26633 MW; B0928A9C7A41D377 CRC64; Query Match 36.6%; Score 45; DB 11; Length 237; Best Local Similarity 63.6%; Pred. No. 25; Mismatches 0; Indels 4; Gaps 0; Matches 7; Conservative 0; Indels 4; Gaps 0;
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3 WRCLIPACRR 13
|||
223 WRGSAFCCRR 233

ULT 35

SH1

Q9XSH1 PRELIMINARY; PRT; 249 AA.
Q9XSH1;
01-NOV-1999 (TRENBLrel. 12, Created)
01-NOV-1999 (TRENBLrel. 12, Last sequence update)
01-OCT-2003 (TRENBLrel. 25, Last annotation update)
Membrane-bound folate binding protein.
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
[1]
SEQUENCE FROM N.A.
TISSUE=Placenta;
Vallet J.L., Smith T.P.L., Sontegard T., Pearson P.L.,
Christenson R.K., Klemcke H.G.;
"Isolation of cDNAs encoding putative secreted and membrane-bound
folate binding proteins from endometrium of swine."
Biol. Reprod. 0:0-0(1999).
EMBL; AF137374; AAD33741.1; -.
InterPro: IPR004269; Folt_chemrecept.
Pfam: PF03024; Folate_rec; 1.
SEQUENCE 249 AA; 28755 MW; 17FAAF2001D6B420 CRC64;
Query Match 36.6%; Score 45; DB 6; Length 249;
Best Local Similarity 50.0%; Pred.No.26;
Matches 8; Conservative 3; Mismatches 3; Indels 2; Gaps 1;
1 FNRCC-LIPACRRN 14
||| : |||:
76 FNRHCGKPKCKRH 91

arch completed: February 18, 2004, 06:09:40
> time : 83 secs

Claim 2; Page 31; 47pp; English.

The rho-conotoxin peptide, rho-TIA, is isolated from the venom duct of the fish hunting cone snail *Conus tulipa*. It contains two disulphide bonds. The rho-conotoxin peptide has selective alpha-1-adrenoceptor antagonist activity. It can be used in a receptor binding assay to test the activity of a molecule as an antagonist of alpha-1-adrenoceptor activity. Rho-TIA is labeled, e.g. with radioactive isotope and used to identify molecules which act at the same site. Antibodies to rho-TIA are useful as therapeutic and diagnostic agents. Rho-conotoxin can be used for the treatment of or prophylaxis of a urinary system disease, e.g. prostatic hyperplasia, cardiovascular disease, e.g. arrhythmia, hypertension or coronary heart failure, a mood disorder, e.g. craving (e.g. smoking craving) and pain, e.g. chronic pain, neuropathic pain or inflammatory pain (all claimed).

Sequence 19 AA;

Query Match 100.0%; Score 123; DB 3; Length 19;
 Best Local Similarity 100.0%; Pred. NO. 4.7e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 FNRCCCLIPACRRNHKKFC 19
 |||||
 1 FNRCCCLIPACRRNHKKFC 19

ULT 2

92228
 AAY92228 standard; peptide; 15 AA.

AAY92228;

10-AUG-2000 (first entry)

Truncated, inactive rho-conotoxin peptide derivative.

Rho-conotoxin; alpha-1-adrenoreceptor; antagonist; hypotensive; cardiant; analgesic; antiarrhythmic; cyrostatic; nootropic; antiinflammatory.

Conus tulipa.
 Synthetic.

Key Location/Qualifiers
 Disulfide-bond 5 /note= "involved in disulphide bond"
 Disulfide-bond 6 /note= "involved in disulphide bond"
 Disulfide-bond 11 /note= "involved in disulphide bond"
 Disulfide-bond 19 /note= "involved in disulphide bond"

WO200020443-A1.

13-APR-2000.

01-OCT-1999; 99WO-AU000843.

02-OCT-1998; 98AU-00006273.

(UYUQ) UNIV QUEENSLAND.

Lewis RJ, Alewood PF, Sharpe IA;

WPI; 2000-303737/26.

Isolated rho-conotoxin peptide used for the treatment of urinary or cardiovascular conditions or diseases, mood disorders or for control of pain or inflammation comprises selective alpha1-adrenoceptor antagonist activity.

PS Disclosure; Page 3; 47pp; English.

XX The rho-conotoxin peptide, rho-TIA (see AAY92227), is isolated from the
 CC venom duct of the fish hunting cone snail *Conus tulipa*. It contains two
 CC disulphide bonds. The rho-conotoxin peptide has selective alpha-1-
 CC adrenoceptor antagonist activity. It can be used in a receptor binding
 CC assay to test the activity of a molecule as an antagonist of alpha-1-
 CC adrenoceptor activity. Rho-TIA is labeled, e.g. with radioactive isotope
 CC and used to identify molecules which act at the same site. Antibodies to
 CC rho-TIA are useful as therapeutic and diagnostic agents. Rho-conotoxin
 CC can be used for the treatment of or prophylaxis of a urinary system
 CC disease, e.g. prostatic hyperplasia, cardiovascular disease, e.g.
 CC arrhythmia, hypertension or coronary heart failure, a mood disorder, e.g.
 CC craving (e.g. smoking craving) and pain, e.g. chronic pain, neuropathic
 CC pain or inflammatory pain (all claimed)

SQ Sequence 15 AA;

Query Match 77.2%; Score 95; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. NO. 1.5e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCLIPACRRNHKKFC 19
 |||||
 Db 1 CCLIPACRRNHKKFC 15

RESULT 3

AAB21635
 ID AAB21635 standard; peptide; 40 AA.

XX AAB21635;

XX 19-JAN-2001 (first entry)

XX Cone snail alpha-conotoxin SEQ ID NO: 398.

XX Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
 KW neuronal nicotinic acetylcholine receptor; cardiovascular disorder;
 KW gastric motility disorder; urinary incontinence; nicotine addiction;
 KW small cell lung carcinoma.

XX *Conus tulipa*.

XX WO200044776-A1.

XX 03-AUG-2000.

XX 28-JAN-2000; 2000WO-US001979.

XX 29-JAN-1999; 99US-0118381P.

XX (UTAH) UNIV UTAH RES FOUND.

XX (COGN-) COGNETIX INC.

XX Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

XX WPI; 2000-505965/45.

XX N-ESDB; AAA89531.

XX alpha-conotoxin polypeptides derived from the venom of cone snails useful
 PT e.g. as neuromuscular blocking agents for use in surgery and for treating
 PT unipolar depression.

XX Claim 39; Page 66; 229pp; English.

XX The present invention relates to a number of alpha-conotoxin peptides and
 CC their coding sequences from a number of different species of cone snail.
 CC These peptides are found in minute quantities in the venom of the snails,
 CC and are targeted at the neuronal nicotinic acetylcholine receptors of the
 CC nervous system. They usually contain two disulphide bonds, which give
 CC them defined conformations, a rarity in molecules this small. The alpha-
 CC conotoxins can be used as neuromuscular blocking agents in surgery, and

For treating disorders regulated at the neuronal nicotinic acetylcholine receptors, including cardiovascular disorders, gastric motility disorders, urinary incontinence, nicotine addiction, mood disorders such as bipolar disorder, unipolar depression, dysthymia and seasonal affective disorder, and small cell lung carcinoma

Sequence 40 AA;

Query Match 45.9%; Score 56.5; DB 3; Length 40;
 Best Local Similarity 55.6%; Pred. No. 3;
 Matches 10; Conservative 1; Mismatches 6; Indels 1; Gaps 1;
 3 WR-CCLPACRRNHKKFC 19
 19 WEGCCSNPACLVNHRFC 35

RESULT 4

321612
 AAB21612 standard; peptide; 24 AA.

AAB21612;

19-JAN-2001 (first entry)

Cone snail alpha-conotoxin SEQ ID NO: 352.

Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
 neuronal nicotinic acetylcholine receptor; cardiovascular disorder;
 gastric motility disorder; urinary incontinence; nicotine addiction;
 small cell lung carcinoma.

Conus obscurus.

WO200044776-A1.

03-AUG-2000.

28-JAN-2000; 2000WO-US001979.

29-JAN-1999; 99US-0118381P.

(UTAH) UNIV UTAH RES FOUND.
 (COGN-) COGNETIX INC.

Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

WPI; 2000-505965/45.
 N-PSDB; AAA89508.

alpha-conotoxin polypeptides derived from the venom of cone snails useful
 e.g. as neuromuscular blocking agents for use in surgery and for treating
 unipolar depression.

Claim 39; Page 60; 229pp; English.

The present invention relates to a number of alpha-conotoxin peptides and
 their coding sequences from a number of different species of cone snail.
 These peptides are found in minute quantities in the venom of the snails,
 and are targeted at the neuronal nicotinic acetylcholine receptors of the
 nervous system. They usually contain two disulphide bonds, which give
 them defined conformations, a rarity in molecules this small. The alpha-
 conotoxins can be used as neuromuscular blocking agents in surgery, and
 for treating disorders regulated at the neuronal nicotinic acetylcholine
 receptors, including cardiovascular disorders, gastric motility
 disorders, urinary incontinence, nicotine addiction, mood disorders such
 as bipolar disorder, unipolar depression, dysthymia and seasonal
 affective disorder, and small cell lung carcinoma

Sequence 24 AA;

Query Match 44.7%; Score 55; DB 3; Length 24;
 Best Local Similarity 53.3%; Pred. No. 3.1;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 5 CCLIPACRRNHKKFC 19
 DB 6 CSHPVCKFNPYKVC 20

RESULT 5

AAB21610
 ID AAB21610 standard; peptide; 38 AA.

XX AC AAB21610;

XX DT 19-JAN-2001 (first entry)

XX DE Cone snail alpha-conotoxin SEQ ID NO: 348.

XX KW Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
 KW neuronal nicotinic acetylcholine receptor; cardiovascular disorder;
 KW gastric motility disorder; urinary incontinence; nicotine addiction;
 KW small cell lung carcinoma.

XX OS Conus musicus.

XX FN WO200044776-A1.

XX PD 03-AUG-2000.

XX PF 28-JAN-2000; 2000WO-US001979.

XX PR 29-JAN-1999; 99US-0118381P.

XX PA (UTAH) UNIV UTAH RES FOUND.

XX PA (COGN-) COGNETIX INC.

XX PI Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

XX DR WPI; 2000-505965/45.

XX DR N-PSDB; AAA89508.

XX alpha-conotoxin polypeptides derived from the venom of cone snails useful
 e.g. as neuromuscular blocking agents for use in surgery and for treating
 unipolar depression.

PS Claim 39; Page 59; 229pp; English.

CC The present invention relates to a number of alpha-conotoxin peptides and
 their coding sequences from a number of different species of cone snail.
 CC These peptides are found in minute quantities in the venom of the snails,
 CC and are targeted at the neuronal nicotinic acetylcholine receptors of the
 CC nervous system. They usually contain two disulphide bonds, which give
 CC them defined conformations, a rarity in molecules this small. The alpha-
 CC conotoxins can be used as neuromuscular blocking agents in surgery, and
 CC for treating disorders regulated at the neuronal nicotinic acetylcholine
 CC receptors, including cardiovascular disorders, gastric motility
 CC disorders, urinary incontinence, nicotine addiction, mood disorders such
 CC as bipolar disorder, unipolar depression, dysthymia and seasonal
 CC affective disorder, and small cell lung carcinoma

XX Sequence 38 AA;

Query Match 44.7%; Score 55; DB 3; Length 38;
 Best Local Similarity 43.8%; Pred. No. 4.5;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 4 RCCLIPACRRNHKKFC 19

DB 19 KCCINDACRSKHPQYC 34

RESULT 6

AAB21637
 ID AAB21637 standard; peptide; 38 AA.

AAB21637;

19-JAN-2001 (first entry)

Cone snail alpha-conotoxin SEQ ID NO: 402.

Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
 neuronal nicotinic acetylcholine receptor; cardiovascular disorder;
 gastric motility disorder; urinary incontinence; nicotine addiction;
 small cell lung carcinoma.

Conus geographus.

WO200044776-A1.

03-AUG-2000.

28-JAN-2000; 2000WO-US001979..

29-JAN-1999; 99US-0118381P.

(UTAH) UNIV UTAH RES FOUND.
 (COGN-) COGNETIX INC.

Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

WPI; 2000-505965/45.

N-PSDB; AAA89425.

alpha-conotoxin polypeptides derived from the venom of cone snails useful
 e.g. as neuromuscular blocking agents for use in surgery and for treating
 unipolar depression.

Claim 39; Page 66; 229pp; English.

The present invention relates to a number of alpha-conotoxin peptides and
 their coding sequences from a number of different species of cone snail.
 These peptides are found in minute quantities in the venom of the snails,
 and are targeted at the neuronal nicotinic acetylcholine receptors of the
 nervous system. They usually contain two disulphide bonds, which give
 them defined conformations, a rarity in molecules this small. The alpha-
 conotoxins can be used as neuromuscular blocking agents in surgery, and
 for treating disorders regulated at the neuronal nicotinic acetylcholine
 receptors, including cardiovascular disorders, gastric motility
 disorders, urinary incontinence, nicotine addiction, mood disorders such
 as bipolar disorder, unipolar depression, dysthymia and seasonal
 affective disorder, and small cell lung carcinoma

Sequence 38 AA;

Query Match 44.3%; Score 54.5; DB 3; Length 38;

Best Local Similarity 50.0%; Pred. No. 5.2;

Matches 9; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

3 WRCLIPACRRNHK-KFC 19

 ||| ||| ||| ||| |||
 19 WRCTIPSCYEKKIKAC 36

SULT 7

B21450

AAB21450 standard; protein; 61 AA.

AAB21450;

19-JAN-2001 (first entry)

Cone snail alpha-conotoxin SEQ ID NO: 107.

Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
 neuronal nicotinic acetylcholine receptor; cardiovascular disorder;
 gastric motility disorder; urinary incontinence; nicotine addiction;

KW small cell lung carcinoma.

OS Conus betulinus.

PN WO200044776-A1.

XX 03-AUG-2000.

XX 28-JAN-2000; 2000WO-US001979.

XX 29-JAN-1999; 99US-0118381P.

XX (UTAH) UNIV UTAH RES FOUND.

XX (COGN-) COGNETIX INC.

XX Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

XX WPI; 2000-505965/45.

XX N-PSDB; AAA89425.

XX alpha-conotoxin polypeptides derived from the venom of cone snails useful
 e.g. as neuromuscular blocking agents for use in surgery and for treating
 unipolar depression.

XX Claim 39; Page 38-39; 229pp; English.

XX The present invention relates to a number of alpha-conotoxin peptides and
 their coding sequences from a number of different species of cone snail.
 These peptides are found in minute quantities in the venom of the snails,
 and are targeted at the neuronal nicotinic acetylcholine receptors of the
 nervous system. They usually contain two disulphide bonds, which give
 them defined conformations, a rarity in molecules this small. The alpha-
 conotoxins can be used as neuromuscular blocking agents in surgery, and
 for treating disorders regulated at the neuronal nicotinic acetylcholine
 receptors, including cardiovascular disorders, gastric motility
 disorders, urinary incontinence, nicotine addiction, mood disorders such
 as bipolar disorder, unipolar depression, dysthymia and seasonal
 affective disorder, and small cell lung carcinoma

XX Sequence 61 AA;

Query Match 42.3%; Score 52; DB 3; Length 61;

Best Local Similarity 53.3%; Pred. No. 16;

Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKFC 19

 ||| ||| ||| ||| |||
 46 CSHPCACAVNHPELC 60

RESULT 8

AAB21440

ID AAB21440 standard; protein; 62 AA.

XX AAB21440;

XX 19-JAN-2001 (first entry)

XX Cone snail alpha-conotoxin SEQ ID NO: 87.

XX Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
 XX neuronal nicotinic acetylcholine receptor; cardiovascular disorder;
 KW gastric motility disorder; urinary incontinence; nicotine addiction;
 KW small cell lung carcinoma.

XX Conus tulipa.

XX WO200044776-A1.

XX 03-AUG-2000.

XX 28-JAN-2000; 2000WO-US001979.

XX

29-JAN-1999; 99US-0118381P.

(UTAH) UNIV UTAH RES FOUND.
(COGN-) COGNETIX INC.

Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

WPI; 2000-505965/45.
N-PSDB; AAA89415.

alpha-conotoxin polypeptides derived from the venom of cone snails useful
e.g. as neuromuscular blocking agents for use in surgery and for treating
unipolar depression.

Claim 39; Page 35-36; 229pp; English.

The present invention relates to a number of alpha-conotoxin peptides and
their coding sequences from a number of different species of cone snail.
These peptides are found in minute quantities in the venom of the snails,
and are targeted at the neuronal nicotinic acetylcholine receptors of the
nervous system. They usually contain two disulphide bonds, which give
them defined conformations, a rarity in molecules this small. The alpha-
conotoxins can be used as neuromuscular blocking agents in surgery, and
for treating disorders regulated at the neuronal nicotinic acetylcholine
receptors, including cardiovascular disorders, gastric motility
disorders, urinary incontinence, nicotine addiction, mood disorders such
as bipolar disorder, unipolar depression, dysthymia and seasonal
affective disorder, and small cell lung carcinoma

Sequence 62 AA;

Query Match 42.3%; Score 52; DB 3; Length 62;
est Local Similarity 53.3%; Pred. No. 16;
atches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19
||| ||| | : |||
44 CCHPACSGNNPEFC 58

UIT 9
21616

AAB21616 standard; peptide; 62 AA.

AAB21616;

19-JAN-2001 (first entry)

Cone snail alpha-conotoxin SEQ ID NO: 360.

Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
neuronal nicotinic acetylcholine receptor; cardiovascular disorder;
gastric motility disorder; urinary incontinence; nicotine addiction;
small cell lung carcinoma.

Conus obscurus.

WO200044776-A1.

03-AUG-2000.

28-JAN-2000; 2000WO-US001979.

29-JAN-1999; 99US-0118381P.

(UTAH) UNIV UTAH RES FOUND.
(COGN-) COGNETIX INC.

Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

WPI; 2000-505965/45.
N-PSDB; AAA89512.

PT alpha-conotoxin polypeptides derived from the venom of cone snails useful
PT e.g. as neuromuscular blocking agents for use in surgery and for treating
PT unipolar depression.

XX Claim 39; Page 61; 229pp; English.

XX The present invention relates to a number of alpha-conotoxin peptides and
CC their coding sequences from a number of different species of cone snail.
CC These peptides are found in minute quantities in the venom of the snails,
CC and are targeted at the neuronal nicotinic acetylcholine receptors of the
CC nervous system. They usually contain two disulphide bonds, which give
CC them defined conformations, a rarity in molecules this small. The alpha-
CC conotoxins can be used as neuromuscular blocking agents in surgery, and
CC for treating disorders regulated at the neuronal nicotinic acetylcholine
CC receptors, including cardiovascular disorders, gastric motility
CC disorders, urinary incontinence, nicotine addiction, mood disorders such
CC as bipolar disorder, unipolar depression, dysthymia and seasonal
CC affective disorder, and small cell lung carcinoma

XX Sequence 62 AA;

Query Match 42.3%; Score 52; DB 3; Length 62;
Best Local Similarity 46.7%; Pred. No. 16;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Oy 5 CCLIPACRRNHKKFC 19

Db 44 CCHPACSGNNREYC 58

RESULT 10

AAB21452

ID AAB21452 standard; protein; 64 AA.

XX AAB21452;

19-JAN-2001 (first entry)

Cone snail alpha-conotoxin SEQ ID NO: 111.

Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
neuronal nicotinic acetylcholine receptor; cardiovascular disorder;
gastric motility disorder; urinary incontinence; nicotine addiction;
small cell lung carcinoma.

OS Conus betulinus.

XX WO200044776-A1.

XX 03-AUG-2000.

XX 28-JAN-2000; 2000WO-US001979.

XX 29-JAN-1999; 99US-0118381P.

XX (UTAH) UNIV UTAH RES FOUND.

XX (COGN-) COGNETIX INC.

XX Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

XX WPI; 2000-505965/45.

XX N-PSDB; AAA89427.

XX alpha-conotoxin polypeptides derived from the venom of cone snails useful
PT e.g. as neuromuscular blocking agents for use in surgery and for treating
PT unipolar depression.

XX Claim 39; Page 39; 229pp; English.

XX The present invention relates to a number of alpha-conotoxin peptides and
CC their coding sequences from a number of different species of cone snail.
CC These peptides are found in minute quantities in the venom of the snails,
CC and are targeted at the neuronal nicotinic acetylcholine receptors of the

nervous system. They usually contain two disulphide bonds, which give them defined conformations, a rarity in molecules this small. The alpha-conotoxins can be used as neuromuscular blocking agents in surgery, and for treating disorders regulated at the neuronal nicotinic acetylcholine receptors, including cardiovascular disorders, gastric motility disorders, urinary incontinence, nicotine addiction, mood disorders such as bipolar disorder, unipolar depression, dysthymia and seasonal affective disorder, and small cell lung carcinoma

Sequence 64 AA;

Query Match 42.3%; Score 52; DB 3; Length 64;
Best Local Similarity 53.3%; Pred. No. 17;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19
||| ||| : :
46 CCSHPACSVNHPCLC 60

MULT 11
321581

AAB21581 standard; peptide; 60 AA.

AAB21581;

19-JAN-2001 (first entry)

Cone snail alpha-conotoxin SEQ ID NO: 290.

Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
neuronal nicotinic acetylcholine receptor; cardiovascular disorder;
gastric motility disorder; urinary incontinence; nicotine addiction;
small cell lung carcinoma.

Conus ammiralis.

WO200044776-A1.

03-AUG-2000.

28-JAN-2000; 2000WO-US001979.

29-JAN-1999; 99US-0118381P.

(UTAH) UNIV UTAH RES FOUND.
(COGN-) COGNEX INC.

Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

WPI; 2000-505965/45.
N-PSDB; AAA89477.

alpha-conotoxin polypeptides derived from the venom of cone snails useful
e.g. as neuromuscular blocking agents for use in surgery and for treating
unipolar depression.

Claim 39; Page 52; 229pp; English.

The present invention relates to a number of alpha-conotoxin peptides and
their coding sequences from a number of different species of cone snail.
These peptides are found in minute quantities in the venom of the snails,
and are targeted at the neuronal nicotinic acetylcholine receptors of the
nervous system. They usually contain two disulphide bonds, which give
them defined conformations, a rarity in molecules this small. The alpha-
conotoxins can be used as neuromuscular blocking agents in surgery, and
for treating disorders regulated at the neuronal nicotinic acetylcholine
receptors, including cardiovascular disorders, gastric motility
disorders, urinary incontinence, nicotine addiction, mood disorders such
as bipolar disorder, unipolar depression, dysthymia and seasonal
affective disorder, and small cell lung carcinoma

Sequence 60 AA;

Query Match 41.5%; Score 51; DB 4; Length 221;

Query Match 41.5%; Score 51; DB 3; Length 60;
Best Local Similarity 46.7%; Pred. No. 22;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Oy 5 CCLIPACRRNHKKFC 19
||| ||| : :
Db 45 CCSYPACNLDHPCLC 59

RESULT 12

ABG04153

ID ASS04153 standard; protein; 221 AA.

AC ABG04153;

DT 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #4144.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

PD 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR N-PSDB; AAS68340.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

PS Claim 20; SEQ ID NO 34512; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have application in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG0377 represent novel human diagnostic
CC patent did not appear in the printed specification. Note: The sequence data for this
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 221 AA;

est Local Similarity 50.0%; Pred. No. 64;
atches 8; Conservative 4; Mismatches 2; Indels 2; Gaps 1;
1 FNNRCC--LIPACRRN 14
||| |::|||::|
81 FNNHCGEMVPACKRH 96

ULT 13
75280
AAR75280 standard; peptide; 18 AA.

AAR75280;

22-DEC-1995 (first entry)

A-lineage conotoxin SL-1 peptide.

Alpha conotoxin; neuromuscular; synapse; signal transmission.

Conus sulcatus.

Key Location/Qualifiers

Misc-difference 7 /label= Pro or OTHER

/note= "Hydroxyproline"

Misc-difference 14 /label= Pro or OTHER

/note= "Hydroxyproline"

Modified-site 15 /note= "Glu, can form a peptide bond via either the alpha

or gamma carboxyl group"

Modified-site 18 /note= "preferably amidated"

WO9511256-A1.

27-APR-1995.

19-OCT-1994; 94WO-US011927.

19-OCT-1993; 93US-00137800.

(UTAH) UNIV UTAH RES FOUND.

Olivera BM, Cruz LJ, Hillyard DR, McIntosh JM, Santos AD;

WPI; 1995-170189/22.

New A-lineage conotoxin peptide(s) - which inhibit synaptic transmission

at the neuromuscular junction or are active against potassium or sodium

channels.

Claim 1; Page 44; 66pp; English.

The kappa-conotoxin, alpha conotoxin and alpha-like conotoxin peptides

all belong to a group of peptides known as the A-lineage conotoxin

peptides. The A lineage conotoxin peptides have a wide variety of

pharmacological uses. The A-lineage conotoxin peptides claimed (AAR75264-

R75293) are useful for the inhibition of synaptic transmission at

neuromuscular junctions by blocking nicotinic acetyl choline receptors

and they also have activity against voltage-gated Na and K channels

Sequence 18 AA;

Query Match 40.7%; Score 50; DB 2; Length 18;

Best Local Similarity 46.7%; Pred. No. 11;

Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19

||| |::|||::|

3 CCSFPACKRYPEMC 17

RESULT 14

AAW12742

ID AAW12742 standard; peptide; 18 AA.

XX AC AAW12742;

XX DT 25-MAR-2003 (revised)

XX DT 16-APR-1997 (first entry)

XX DE A-lineage conotoxin peptide SL-1.

XX KW Polymerase chain reaction; PCR; primer; amplify; conotoxin; Conus;

XX KW inhibitor; synaptic transmission; neuromuscular junction; sodium channel;

XX KW nicotinic acetylcholine receptor; potassium channel; muscle relaxant;

XX KW myasthenia gravis; small cell lung cancer; therapy.

XX OS Conus sulcatus.

XX PH Key Location/Qualifiers

FT Modified-site 7 /note= "optionally hydroxylated"

FT Modified-site 14 /note= "optionally hydroxylated"

FT Modified-site 15 /note= "optionally gamma-carboxylated"

FT Modified-site 18 /note= "amidated"

XX US5589340-A.

31-DEC-1996.

07-JUN-1995; 95US-00477383.

29-JUN-1993; 93US-00084848.

19-OCT-1993; 93US-00137800.

(UTAH) UNIV UTAH RES FOUND.

Santos AD, Hillyard DR, McIntosh JM, Olivera BM, Cruz LJ;

WPI; 1997-076840/07.

Identifying nucleic acid encoding A-lineage conotoxin peptide(s) by

amplification - uses primers corresponding to conserved regions in the

signal sequence and 3'-untranslated regions, useful e.g. in treatment of

small cell lung cancer.

Disclosure; Col 5; 36pp; English.

AAW12726-W12769 represent conotoxin peptides. This sequence represents

the A-lineage conotoxin SL-1 peptide isolated from Conus sulcatus. These

sequences are identified using the method of the invention. The method of

the invention is for identifying DNA encoding A-lineage conotoxin

peptides by subjecting Conus nucleic acid to amplification with primer

sequences (see AAR59714 and AAR59715). The primers are specific for the

signal sequence and 3'-untranslated (3'UTR) regions of the conotoxin

gene, which are highly homologous between conotoxins, and are therefore

suitable sites for detection. A-lineage conotoxins include alpha-

conotoxins, and kappa-conotoxins. Alpha-conotoxins are powerful

inhibitors of synaptic transmission at the neuromuscular junction, and

are usually nicotinic acetylcholine receptor blockers. Kappa-conotoxins

act on the voltage sensitive sodium and potassium channels. The

conotoxins identified can be used as muscle relaxants in the diagnosis

of myasthenia gravis, and for the treatment or diagnosis of small cell

lung cancer. For the treatment of small cell lung cancer, the conotoxin

peptides act by binding to the nicotinic receptors, and thereby blocking

the nicotine/cytosine stimulated release of the mitogen 5-

hydroxytryptamine. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 18 AA;

Query Match 40.7%; Score 50; DB 2; Length 18;
 est Local Similarity 46.7%; Pred. No. 11;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19
 ||||| : :
 3 CCSPACKKVRPEMC 17

ULT 15

21625

AAB21625 standard; peptide; 37 AA.

AAB21625;

19-JAN-2001 (first entry)

Cone snail alpha-conotoxin SEQ ID NO: 378.

Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
 neuronal nicotinic acetylcholine receptor; cardiovascular disorder;
 gastric motility disorder; urinary incontinence; nicotine addiction;
 small cell lung carcinoma.

Conus purpurascens.

WC200044776-A1.

03-AUG-2000.

28-JAN-2000; 2000WC-US001979.

29-JAN-1999; 99US-0118381P.

(UTAH) UNIV UTAH RES FOUND.

(COGN-) COGNETIX INC.

Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

WPI; 2000-505965/45.

N-PSDB; AAA89521.

alpha-conotoxin polypeptides derived from the venom of cone snails useful
 e.g. as neuromuscular blocking agents for use in surgery and for treating
 unipolar depression.

Claim 39; Page 63; 229pp; English.

The present invention relates to a number of alpha-conotoxin peptides and
 their coding sequences from a number of different species of cone snail.
 These peptides are found in minute quantities in the venom of the snails,
 and are targeted at the neuronal nicotinic acetylcholine receptors of the
 nervous system. They usually contain two disulphide bonds, which give
 them defined conformations, a rarity in molecules this small. The alpha-
 conotoxins can be used as neuromuscular blocking agents in surgery, and
 for treating disorders regulated at the neuronal nicotinic acetylcholine
 receptors, including cardiovascular disorders, gastric motility
 disorders, urinary incontinence, nicotine addiction, mood disorders such
 as bipolar disorder, unipolar depression, dysthymia and seasonal
 affective disorder, and small cell lung carcinoma

Sequence 37 AA;

Query Match 40.7%; Score 50; DB 3; Length 37;

Best Local Similarity 53.3%; Pred. No. 19;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19

||||| : :||

19 CCTNPACLVNIRFC 33

SULT 16

AAB21622

ID AAB21622 standard; peptide; 40 AA.

AC AAB21622;

DT 19-JAN-2001 (first entry)

XX DE Cone snail alpha-conotoxin SEQ ID NO: 372.

XX KW Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
 KW neuronal nicotinic acetylcholine receptor; cardiovascular disorder;
 KW gastric motility disorder; urinary incontinence; nicotine addiction;
 KW small cell lung carcinoma.

XX OS Conus purpurascens.

XX FN WC200044776-A1.

XX PD 03-AUG-2000.

XX PF 28-JAN-2000; 2000WC-US001979.

XX PR 29-JAN-1999; 99US-0118381P.

XX PA (UTAH) UNIV UTAH RES FOUND.

XX PA (COGN-) COGNETIX INC.

XX PI Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

XX DR WPI; 2000-505965/45.

XX DR N-PSDB; AAA89518.

XX alpha-conotoxin polypeptides derived from the venom of cone snails useful
 e.g. as neuromuscular blocking agents for use in surgery and for treating
 unipolar depression.

XX PS Claim 39; Page 62; 229pp; English.

XX The present invention relates to a number of alpha-conotoxin peptides and
 their coding sequences from a number of different species of cone snail.
 These peptides are found in minute quantities in the venom of the snails,
 and are targeted at the neuronal nicotinic acetylcholine receptors of the
 nervous system. They usually contain two disulphide bonds, which give
 them defined conformations, a rarity in molecules this small. The alpha-
 conotoxins can be used as neuromuscular blocking agents in surgery, and
 for treating disorders regulated at the neuronal nicotinic acetylcholine
 receptors, including cardiovascular disorders, gastric motility
 disorders, urinary incontinence, nicotine addiction, mood disorders such
 as bipolar disorder, unipolar depression, dysthymia and seasonal
 affective disorder, and small cell lung carcinoma

XX Sequence 40 AA;

Query Match 40.7%; Score 50; DB 3; Length 40;

Best Local Similarity 53.3%; Pred. No. 21;

Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19

||||| : :||

DB 22 CCNPACTLVNHLMEC 36

RESULT 17

AAB21443

ID AAB21443 standard; protein; 65 AA.

XX AC AAB21443;

XX DT 19-JAN-2001 (first entry)

XX DE Cone snail alpha-conotoxin SEQ ID NO: 93.

XX KW Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;

neuronal nicotinic acetylcholine receptor; cardiovascular disorder;
gastric motility disorder; urinary incontinence; nicotine addiction;
small cell lung carcinoma.

Conus sulcatus.

WC2000044776-A1.

03-AUG-2000.

28-JAN-2000; 2000WO-US001979.

29-JAN-1999; 99US-0118381P.

(UTAH) UNIV UTAH RES FOUND.
(COGN-) COGNETIX INC.

Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

WPI; 2000-505965/45.
N-PSDB; AAA89418.

alpha-conotoxin polypeptides derived from the venom of cone snails useful
e.g. as neuromuscular blocking agents for use in surgery and for treating
unipolar depression.

Claim 39; Page 36-37; 229pp; English.

The present invention relates to a number of alpha-conotoxin peptides and
their coding sequences from a number of different species of cone snail.
These peptides are found in minute quantities in the venom of the snails,
and are targeted at the neuronal nicotinic acetylcholine receptors of the
nervous system. They usually contain two disulphide bonds, which give
them defined conformations, a rarity in molecules this small. The alpha-
conotoxins can be used as neuromuscular blocking agents in surgery, and
for treating disorders regulated at the neuronal nicotinic acetylcholine
receptors, including cardiovascular disorders, gastric motility
disorders, urinary incontinence, nicotine addiction, mood disorders such
as bipolar disorder, unipolar depression, dysthymia and seasonal
affective disorder, and small cell lung carcinoma

Sequence 65 AA;

Query Match 40.7%; Score 50; DB 3; Length 65;
Best Local Similarity 46.7%; Pred. No. 31;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRHHKFC 19
||| ||||| :
47 CCSFPACRKYRPMC 61

SULT 18

B88269

ABB88269 standard; protein; 76 AA.

ABB88269;

24-MAY-2002 (first entry)

C radiatus mu-conopeptide R3-1 propeptide.

Mu-conopeptide; snail; venom; voltage-gated sodium channel; analgesic;
anaesthetic; neuromuscular blocking agent; neuroprotective; pain;
cerebroprotective; anticonvulsant; antiaging; antidiabetic;
cardiovascular; vasotropic; cardiac; tranquilizer; antimigraine;
neurodegenerative disease; neuromuscular disorder.

Conus radiatus.

WC200207678-A2.

31-JAN-2002.

XX 23-JUL-2001; 2001WO-US023125.
XX 21-JUL-2000; 2000US-0219619P.
PR 03-NOV-2000; 2000US-0245157P.
PR 29-JAN-2001; 2001US-0264319P.
PR 21-MAR-2001; 2001US-0277270P.
XX (UTAH) UNIV UTAH RES FOUND.
PA (COGN-) COGNETIX INC.
XX Olivera BM, McIntosh JM, Garrett JE, Watkins M, Cruz LJ, Shon K;
PI Jacobsen R, Jones RM, Cartier GS, Shen GS;
XX WPI; 2002-217020/27.
DR N-PSDB; ABL88542.
XX New mu-conopeptides useful for treating disorders associated with voltage
PT -gated sodium channels, e.g. stroke or pain, as neuromuscular blocking
PT agents, as local anesthetic agents, as analgesic agents and as
PT neuroprotective agents.

Claim 9; Page 52; 231pp; English.

The present invention relates to mu-conopeptides derived from snails,
which can be in the treatment of disorders associated with voltage-gated
ion channels. These may include neurodegenerative disorders such as
CC amyotrophic lateral sclerosis, neuromuscular disorders, post-operative or
CC severe chronic pain, stroke, trigeminal neuralgia, diabetic neuropathy,
CC post-herpetic neuralgia, neuronal pain and phantom limb, burn pain,
CC epilepsy, for reducing neurotoxic injury associated with hypoxia, anoxia
or ischaemia which typically follows stroke, cerebrovascular accident,
CC brain or spinal cord trauma, myocardial infarct, physical trauma,
CC drowning, suffocation, perinatal asphyxia, or hypoglycaemic events, for
CC providing muscle relaxation, treating essential blepharospasm and other
CC forms of focal dystonia, and for anti-wrinkle use. The present sequence
CC is a mu-conopeptide preprotein of the invention

SQ Sequence 76 AA;

Query Match 40.7%; Score 50; DB 5; Length 76;
Best Local Similarity 61.5%; Pred. No. 35;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 NWRCCILIPACRRN 14
||| ||||| :
Db 59 NLRLLCPVPCRRN 71

RESULT 19

AAR75275

ID AAR75275 standard; peptide; 16 AA.

XX AAR75275;

XX 27-AUG-2003 (revised)

DT 21-DEC-1995 (first entry)

XX A-lineage conotoxin BN-2 peptide.

XX Conotoxin; neuromuscular; synapse; signal transmission; inhibitor.

XX Conus bandanus.

XX Key Location/Qualifiers

FT Misc-difference 6 /label= Pro or OTHER

FT /note= "Hydroxyproline"

FT Misc-difference 13 /label= Pro or OTHER

FT /note= "Hydroxyproline"

FT Modified-site 16 /note= "preferably amidated"

FT

WO9511256-A1.
27-APR-1995.
19-OCT-1994; 94WO-US011927.
19-OCT-1993; 93US-00137800.
(UTAH) UNIV UTAH RES FOUND.
Olivera BM, Cruz LJ, Hillyard DR, McIntosh JM, Santos AD;
WPI; 1995-170189/22.
New A-lineage conotoxin peptide(s) - which inhibit synaptic transmission at the neuromuscular junction or are active against potassium or sodium channels.
Claim 1; Page 42; 66pp; English.
The kappa-conotoxin, alpha conotoxin and alpha-like conotoxin peptides all belong to a group of peptides known as the A-lineage conotoxin peptides. The A-lineage conotoxin peptides have a wide variety of pharmacological uses. The A-lineage conotoxin peptides claimed (AAR75264-75293) are useful for the inhibition of synaptic transmission at neuromuscular junctions by blocking nicotinic acetyl choline receptors and they also have activity against voltage-gated Na and K channels.
(Updated on 27-AUG-2003 to correct OS field.)
Sequence 16 AA;
Query Match 39.8%; Score 49; DB 2; Length 16;
Best Local Similarity 46.7%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
5 CCLIPACRRNHKKFC 19
|||:::
2 CCHTPACHVSHPELC 16
SULT 20
W24882
AAW24882 standard; peptide; 16 AA.
AAW24882;
25-MAR-2003 (revised)
15-OCT-1997 (first entry)
Predatory cone snail venom alpha-conotoxin BN-2.
Conotoxin; venom; predatory; cone snail; Conus; A-lineage; inhibitor;
synaptic transmission; neuromuscular junction; block; alpha-conotoxin;
nicotinic acetylcholine receptor; kappa-conotoxin;
voltage-sensitive potassium CHANNEL; sodium channel.
Conus bandanus.
Key Location/Qualifiers
Modified-site 6
/note= "optionally may be 4Hyp"
Modified-site 13
/note= "optionally may be 4Hyp"
Modified-site 16
/note= "amidated C-terminus"
US5633347-A.
27-MAY-1997.
07-JUN-1995; 95US-00480750.
WO9511256-A1.
27-APR-1995.
19-OCT-1994; 94WO-US011927.
19-OCT-1993; 93US-00137800.
(UTAH) UNIV UTAH RES FOUND.
Olivera BM, Cruz LJ, Hillyard DR, McIntosh JM, Santos AD;
WPI; 1995-170189/22.
New A-lineage conotoxin peptide(s) - which inhibit synaptic transmission at the neuromuscular junction or are active against potassium or sodium channels.
Claim 1; Page 42; 66pp; English.
The kappa-conotoxin, alpha conotoxin and alpha-like conotoxin peptides all belong to a group of peptides known as the A-lineage conotoxin peptides. The A-lineage conotoxin peptides have a wide variety of pharmacological uses. The A-lineage conotoxin peptides claimed (AAR75264-75293) are useful for the inhibition of synaptic transmission at neuromuscular junctions by blocking nicotinic acetyl choline receptors and they also have activity against voltage-gated Na and K channels.
(Updated on 27-AUG-2003 to correct OS field.)
Sequence 16 AA;
Query Match 39.8%; Score 49; DB 2; Length 16;
Best Local Similarity 46.7%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
5 CCLIPACRRNHKKFC 19
|||:::
2 CCHTPACHVSHPELC 16
SULT 20
W24882
AAW24882 standard; peptide; 16 AA.
AAW24882;
25-MAR-2003 (revised)
15-OCT-1997 (first entry)
Predatory cone snail venom alpha-conotoxin BN-2.
Conotoxin; venom; predatory; cone snail; Conus; A-lineage; inhibitor;
synaptic transmission; neuromuscular junction; block; alpha-conotoxin;
nicotinic acetylcholine receptor; kappa-conotoxin;
voltage-sensitive potassium CHANNEL; sodium channel.
Conus bandanus.
Key Location/Qualifiers
Modified-site 6
/note= "optionally may be 4Hyp"
Modified-site 13
/note= "optionally may be 4Hyp"
Modified-site 16
/note= "amidated C-terminus"
US5633347-A.
27-MAY-1997.
07-JUN-1995; 95US-00480750.
WO9511256-A1.
27-APR-1995.
19-OCT-1994; 94WO-US011927.
19-OCT-1993; 93US-00137800.
(UTAH) UNIV UTAH RES FOUND.
Olivera BM, Cruz LJ, Hillyard DR, McIntosh JM, Santos AO, Olivera BM;
WPI; 1997-309336/28.
New kappa-conotoxin peptide(s) - present in venom of fish-hunting cone snail.
Disclosure; Col 5; 37pp; English.
The peptides AAW24878-W24900 represent novel toxin peptides isolated from the venom of various predatory cone snails of the genus Conus. The peptides are A-lineage conotoxin peptides which fall into 3 groups dependent on their amino acid sequences: (i) alpha-3/5 have a core sequence CXXXXXXXXC where X is any amino acid; (ii) alpha-4/7 have a core sequence CXXXXXXXCXCC; and (iii) kappa-7/21/3 have the core sequence CXXXXXXXCXCCXXC. The peptide presented here was isolated from Conus bandanus and falls into the alpha-4/7 category. Alpha-conotoxin peptides are potent inhibitors of synaptic transmission at the neuromuscular junction by blocking nicotinic acetylcholine receptors, whereas kappa-conotoxins have activities against voltage-sensitive potassium or sodium channels. (Updated on 25-MAR-2003 to correct PF field.)
Sequence 16 AA;
Query Match 39.8%; Score 49; DB 2; Length 16;
Best Local Similarity 46.7%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
5 CCLIPACRRNHKKFC 19
|||:::
2 CCHTPACHVSHPELC 16
RESULT 21
AAW12737
ID AAW12737 standard; peptide; 16 AA.
XX
AC AAW12737;
XX
DT 25-MAR-2003 (revised)
DT 16-APR-1997 (first entry)
XX
DE A-lineage conotoxin peptide BN-2.
XX
KW Polymerase chain reaction; PCR; primer; amplify; conotoxin; Conus;
KW inhibitor; synaptic transmission; neuromuscular junction; sodium channel;
KW nicotinic acetylcholine receptor; potassium channel; muscle relaxant;
KW myasthenia gravis; small cell lung cancer; therapy.
XX
OS Conus bandanus.
XX
PH Key Location/Qualifiers
FT Modified-site 6
/note= "optionally hydroxylated"
FT Modified-site 13
/note= "optionally hydroxylated"
FT Modified-site 15
/note= "amidated"
XX
PN US5589340-A.
XX
PD 31-DEC-1996.
XX
PF 07-JUN-1995; 95US-00477383.
XX
PR 29-JUN-1993; 93US-00084848.
PR 19-OCT-1993; 93US-00137800.

(UTAH) UNIV UTAH RES FOUND.

Santos AD, Hillyard DR, McIntosh JM, Olivera BM, Cruz LJ;

WPI; 1997-076840/07.

Identifying nucleic acid encoding A-lineage conotoxin peptide(s) by amplification - uses primers corresponding to conserved regions in the signal sequence and 3'-untranslated regions, useful e.g. in treatment of small cell lung cancer.

Disclosure; Col 5; 36pp; English.

AAW12726-W12769 represent conotoxin peptides. This sequence represents the A-lineage conotoxin BN-2 peptide isolated from *Conus bandanus*. These sequences are identified using the method of the invention. The method of the invention is for identifying DNA encoding A-lineage conotoxin peptides by subjecting *Conus* nucleic acid to amplification with primer sequences (see AAT59714 and AAT59715). The primers are specific for the signal sequence and 3'-untranslated (3'UTR) regions of the conotoxin gene, which are highly homologous between conotoxins, and are therefore suitable sites for detection. A-lineage conotoxins include alpha-conotoxins, and kappa-conotoxins. Alpha-conotoxins are powerful inhibitors of synaptic transmission at the neuromuscular junction, and are usually nicotinic acetylcholine receptor blockers. Kappa-conotoxins act on the voltage sensitive sodium and potassium channels. The conotoxins identified can be used as muscle relaxants, in the diagnosis of myasthenia gravis, and for the treatment or diagnosis of small cell lung cancer. For the treatment of small cell lung cancer, the conotoxin peptides act by binding to the nicotinic receptors, and thereby blocking the nicotine/cytosine stimulated release of the mitogen 5-hydroxytryptamine. (Updated on 25-MAR-2003 to correct PF field.)

Sequence 16 AA;

Query Match 39.8%; Score 49; DB 2; Length 16;
Best Local Similarity 46.7%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
5 CCLIPACRRNHKKFC 19
2 CCTHPACHVSHPELC 16

SULT 22
p60018
ABP60018 standard; peptide; 16 AA.

ABP60018;

24-FEB-2003 (first entry)

Alpha-conotoxin peptide An1.1.

Alpha-conotoxin; cerebroprotective; analgesic; anticonvulsant; neuroleptic; antiparkinsonian; cyostatic; nootropic; neuroprotective; neuronal nicotinic acetylcholine receptor; NACHR; inhibitor; stroke; pain; cancer related pain; post-surgical pain; oral pain; referred trigeminal neuralgia; post-herpetic neuralgia; phantom limb pain; fibromyalgia; reflex sympathetic dystrophy; rheumatoid arthritis; inflammatory arthritis; neurogenic pain; neuropathic pain; epilepsy; nicotine addiction; schizophrenia; Parkinson's disease; small cell lung carcinoma; Alzheimer's disease; nerve injury.

Conus anemone.

Key Location/Qualifiers

Modified-site 16

/note= "C-terminal amide"

WO200279236-A1.

XX 10-OCT-2002.
XX 28-MAR-2002; 2002WO-AU000411.
XX 29-MAR-2001; 2001AU-00004094.
XX (LIVE/) LIVETT B.
XX (KHAL/) KHALIL Z.
XX (GAYL/) GAYLER K.
XX (DOWN/) DOWN J.
XX Livett B, Khalil Z, Gayler K, Down J;
XX WPI; 2003-103260/09.
XX New alpha-conotoxin-like peptides that inhibit the activity of neuronal
XX nicotinic acetylcholine receptor, useful for treating stroke, pain,
XX schizophrenia, Parkinson's disease, small cell lung carcinoma or
XX Alzheimer's disease.
XX Claim 9; Page 57; 87pp; English.
XX The invention relates to an isolated alpha-conotoxin-like peptide
XX sequence. The activity of peptides of the invention may be described as
XX cerebroprotective, analgesic, anticonvulsant, neuroleptic,
XX antiparkinsonian, cyostatic, nootropic and neuroprotective. Peptides of
XX the invention are neuronal nicotinic acetylcholine receptor (NACHR)
XX inhibitors. The alpha-conotoxin-like peptide is useful for treating a
XX condition mediated by a neuronal nicotinic acetylcholine receptor, e.g.
XX stroke, pain (e.g. cancer related pain, post-surgical pain, oral or
XX dental pain, referred trigeminal neuralgia, post-herpetic neuralgia,
XX phantom limb pain, fibromyalgia, reflex sympathetic dystrophy, pain
XX associated with inflammatory conditions, rheumatoid arthritis or
XX inflammatory arthritis, or pain resulting from conditions associated with
XX neurogenic or neuropathic pain), epilepsy, nicotine addiction,
XX schizophrenia, Parkinson's disease, small cell lung carcinoma, or
XX Alzheimer's disease. The alpha-conotoxin-like peptide is also useful for
XX accelerating recovery from nerve injury. The peptides are also useful as
XX research reagents for investigating nicotinic acetylcholine receptor
XX physiology and pharmacology. The current sequence represents an alpha-
XX conotoxin peptide of the invention that has been designated An1.1
SQ Sequence 16 AA;
Query Match 39.8%; Score 49; DB 6; Length 16;
Best Local Similarity 46.7%; Pred. No. 13;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 5 CCLIPACRRNHKKFC 19
DB 2 CCHPACVANNQDYC 16
||| ||| |::|
RESULT 23
ABG99820 ID ABG99820 standard; peptide; 17 AA.
XX AC ABG99820;
XX 17-JAN-2003 (first entry)
XX DT
XX DE
XX Conus sp conotoxin-associated peptide SEQ ID 605.
XX KW Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;
XX ligand-gated ion channel modulator; pain-relief.
XX OS Conus bandanus.
XX PN WO200264740-A2.
XX 22-AUG-2002.
XX

11-FEB-2002; 2002WO-US003887.

09-FEB-2001; 2001US-0267408P.

(COGN-) COGNETIX INC.

(UTAH) UNIV UTAH RES FOUND.

Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;
Grilley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;

WPI; 2002-706921/76.

New cone snail conotoxin peptides, useful as a pain reliever for alleviating pain in an individual suffering from pain or who is about to be subjected to a pain-causing event, or for treating voltage-gated ion channel disorders.

Claim 1; Page 298-299; 305pp; English.

This invention describes novel conotoxin peptides from the cone snail, genus *Conus* which have analgesic activity and can act as a voltage-gated ion channel modulator or a ligand-gated ion channel modulator. The conotoxin peptide is useful as a pain-relieving agent for alleviating pain in an individual who is either exhibiting pain or is about to be subjected to a pain-causing event. The conotoxin peptide is also useful for treating or preventing disorders associated with voltage-gated ion channel disorders, ligand-gated ion channel disorders or receptor disorders. The radio-labeled conotoxin peptide is also useful for characterizing a new site on these receptors or channels, and for screening and identifying novel small molecules that interact with the above-mentioned channels or receptors, which are monoamine transporters. ABG9360-ABG99853 represent the conotoxin protein and peptides described in the disclosure of the invention

Sequence 17 AA;

Query Match 39.8%; Score 49; DB 5; Length 17;

Best Local Similarity 46.7%; Pred. No. 14;

Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKFC 19

3 CCTHPACHVSHPELC 17

SULT 24

B21436

AB21436 standard; peptide; 18 AA.

AB21436;

19-JAN-2001 (first entry)

Cone snail alpha-conotoxin SEQ ID NO: 79.

Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder; neuronal nicotinic acetylcholine receptor; cardiovascular disorder; gastric motility disorder; urinary incontinence; nicotine addiction; small cell lung carcinoma.

Conus bandanus.

WO200044776-A1.

03-AUG-2000.

28-JAN-2000; 2000WO-US001979.

29-JAN-1999; 99US-0118381P.

(UTAH) UNIV UTAH RES FOUND.

(COGN-) COGNETIX INC.

Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

WPI; 2000-505965/45.

N-PSDB; AAA89411.

alpha-conotoxin polypeptides derived from the venom of cone snails useful e.g. as neuromuscular blocking agents for use in surgery and for treating unipolar depression.

Claim 39; Page 34; 229pp; English.

The present invention relates to a number of alpha-conotoxin peptides and their coding sequences from a number of different species of cone snails. These peptides are found in minute quantities in the venom of the snails, and are targeted at the neuronal nicotinic acetylcholine receptors of the nervous system. They usually contain two disulphide bonds which give them defined conformations, a rarity in molecules this small. The alpha-conotoxins can be used as neuromuscular blocking agents in surgery, and for treating disorders regulated at the neuronal nicotinic acetylcholine receptors, including cardiovascular disorders, gastric motility disorders, urinary incontinence, nicotine addiction, mood disorders such as bipolar disorder, unipolar depression, dysthymia and seasonal affective disorder, and small cell lung carcinoma

Sequence 18 AA;

Query Match 39.8%; Score 49; DB 3; Length 18;

Best Local Similarity 46.7%; Pred. No. 14;

Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKFC 19

3 CCTHPACHVSHPELC 17

RESULT 25

AB21617

ID AAB21617 standard; peptide; 25 AA.

AC AAB21617;

19-JAN-2001 (first entry)

Cone snail alpha-conotoxin SEQ ID NO: 362.

Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder; neuronal nicotinic acetylcholine receptor; cardiovascular disorder; gastric motility disorder; urinary incontinence; nicotine addiction; small cell lung carcinoma.

Conus omaria.

WO200044776-A1.

03-AUG-2000.

28-JAN-2000; 2000WO-US001979.

29-JAN-1999; 99US-0118381P.

(UTAH) UNIV UTAH RES FOUND.

(COGN-) COGNETIX INC.

Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

WPI; 2000-505965/45.

N-PSDB; AAA89513.

alpha-conotoxin polypeptides derived from the venom of cone snails useful e.g. as neuromuscular blocking agents for use in surgery and for treating unipolar depression.

Claim 39; Page 61; 229pp; English.

The present invention relates to a number of alpha-conotoxin peptides and their coding sequences from a number of different species of cone snail. These peptides are found in minute quantities in the venom of the snails, and are targeted at the neuronal nicotinic acetylcholine receptors of the nervous system. They usually contain two disulphide bonds, which give them defined conformations, a rarity in molecules this small. The alpha-conotoxins can be used as neuromuscular blocking agents in surgery, and for treating disorders regulated at the neuronal nicotinic acetylcholine receptors, including cardiovascular disorders, gastric motility disorders, urinary incontinence, nicotine addiction, mood disorders such as bipolar disorder, unipolar depression, dysthymia and seasonal affective disorder, and small cell lung carcinoma

Sequence 25 AA;

Query Match 39.8%; Score 49; DB 3; Length 25;
Best Local Similarity 46.7%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19
||| ||| :| :|
7 CCSYPDCGANHPEIC 21

|||| 26

399639
ABG99639 standard; protein; 60 AA.

ABG99639;

17-JAN-2003 (first entry)

Conus sp conotoxin-associated protein SEQ ID 409.

Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;
ligand-gated ion channel modulator; pain-relief.

Conus bandanus.

WO200264740-A2.

22-AUG-2002.

11-FEB-2002; 2002WO-US003887.

09-FEB-2001; 2001US-026740BP.

(COGN-) COGNETIX INC.

(UTAH) UNIV UTAH RES FOUND.

Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;
Grille M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;

WPI; 2002-706921/76.
N-PSDB; ABX04955.

New cone snail conotoxin peptides, useful as a pain reliever for
alleviating pain in an individual suffering from pain or who is about to
be subjected to a pain-causing event, or for treating voltage-gated ion
channel disorders.

Claim 1; Page 257; 305pp; English.

This invention describes novel conotoxin peptides from the cone snail,
genus Conus which have analgesic activity and can act as a voltage-gated
ion channel modulator or a ligand-gated ion channel modulator. The
conotoxin peptide is useful as a pain-relieving agent for alleviating
pain in an individual who is either exhibiting pain or is about to be
subjected to a pain-causing event. The conotoxin peptide is also useful
for treating or preventing disorders associated with voltage-gated ion
channel disorders, ligand-gated ion channel disorders or receptor
disorders. The radiolabeled conotoxin peptide is also useful for

CC characterising a new site on these receptors or channels, and for
CC screening and identifying novel small molecules that interact with the
CC above-mentioned channels or receptors, which are monoamine transporters.
CC ABG99639-ABG99853 represent the conotoxin protein and peptides described
CC in the disclosure of the invention

XX Sequence 60 AA;

Query Match 39.8%; Score 49; DB 5; Length 60;

Best Local Similarity 46.7%; Pred. No. 39;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19

||| ||| :| :|
DB 45 CCHPACHVSHPELC 59

RESULT 27

AA21431
ID AA21431 standard; protein; 61 AA.

XX AC AA21431;

XX 19-JAN-2001 (first entry)

XX Cone snail alpha-conotoxin SEQ ID NO: 69.

XX Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
KW neuronal nicotinic acetylcholine receptor; cardiovascular disorder;
KW gastric motility disorder; urinary incontinence; nicotine addiction;
KW small cell lung carcinoma.

XX Conus textile.

XX WO200044776-A1.

XX 03-AUG-2000.

XX 28-JAN-2000; 2000WO-US001979.

XX 29-JAN-1999; 99US-0118381P.

XX (UTAH) UNIV UTAH RES FOUND.

XX (COGN-) COGNETIX INC.

XX Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

XX WPI; 2000-505965/45.

XX N-PSDB; AA89406.

PT alpha-conotoxin polypeptides derived from the venom of cone snails useful
e.g. as neuromuscular blocking agents for use in surgery and for treating
unipolar depression.

PS Claim 39; Page 33; 229pp; English.

XX The present invention relates to a number of alpha-conotoxin peptides and
their coding sequences from a number of different species of cone snail.
CC These peptides are found in minute quantities in the venom of the snails,
CC and are targeted at the neuronal nicotinic acetylcholine receptors of the
CC nervous system. They usually contain two disulphide bonds, which give
CC them defined conformations, a rarity in molecules this small. The alpha-
CC conotoxins can be used as neuromuscular blocking agents in surgery, and
CC for treating disorders regulated at the neuronal nicotinic acetylcholine
CC receptors, including cardiovascular disorders, gastric motility
CC disorders, urinary incontinence, nicotine addiction, mood disorders such
CC as bipolar disorder, unipolar depression, dysthymia and seasonal
CC affective disorder, and small cell lung carcinoma

XX Sequence 61 AA;

Query Match 39.8%; Score 49; DB 3; Length 61;

Best Local Similarity 43.8%; Pred. No. 40;

Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

4 RCCLIPACRHHKFC 19
:|||||:|
45 QCCSHPCNVDPHPEIC 60

SULT 28
B21433
AAB21433 standard; protein; 61 AA.
AAB21433;
19-JAN-2001 (first entry)
Cone snail alpha-conotoxin SEQ ID NO: 73.
Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
neuronal nicotinic acetylcholine receptor; cardiovascular disorder;
gastric motility disorder; urinary incontinence; nicotine addiction;
small cell lung carcinoma.
Conus radiatus.
WO200044776-A1.
03-AUG-2000.
28-JAN-2000; 2000WO-US001979.
29-JAN-1999; 99US-0118381P.
(UTAH) UNIV UTAH RES FOUND.
(COGN-) COGNETIX INC.
Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;
WPI; 2000-505965/45.
N-PSDB; AAB89408.
alpha-conotoxin polypeptides derived from the venom of cone snails useful
e.g. as neuromuscular blocking agents for use in surgery and for treating
unipolar depression.
Claim 39; Page 33-34; 229pp; English.
The present invention relates to a number of alpha-conotoxin peptides and
their coding sequences from a number of different species of cone snail.
These peptides are found in minute quantities in the venom of the snails,
and are targeted at the neuronal nicotinic acetylcholine receptors of the
nervous system. They usually contain two disulphide bonds, which give
them defined conformations, a rarity in molecules this small. The alpha-
conotoxins can be used as neuromuscular blocking agents in surgery, and
for treating disorders regulated at the neuronal nicotinic acetylcholine
receptors, including cardiovascular disorders, gastric motility
disorders, urinary incontinence, nicotine addiction, mood disorders such
as bipolar disorder, unipolar depression, dysthymia and seasonal
affective disorder, and small cell lung carcinoma
Sequence 61 AA;
Query Match 39.8%; Score 49; DB 3; Length 61;
Best Local Similarity 43.8%; Pred. No. 40;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
4 RCCLIPACRHHKFC 19
:|||||:|
45 QCCSHPCNVDPHPEIC 60

SULT 29
G11969
ABG11969 standard; protein; 747 AA.

XX ABG11969;
XX 18-FEB-2002 (first entry)
XX Novel human diagnostic protein #11960.
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX Homo sapiens.
XX WO200175067-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US008631.
XX 31-MAR-2000; 2000US-00540217.
XX 23-AUG-2000; 2000US-00849167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX N-PSDB; AAS76156.
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX Claim 20; SEQ ID NO 42328; 103pp; English.
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activity. The
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
XX amino acid sequences of the invention. Note: The sequence data for this
XX patent did not appear in the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 747 AA;
XX Query Match 39.8%; Score 49; DB 4; Length 747;
XX Best Local Similarity 66.7%; Pred. No. 3.2e+02;
XX Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 FNRRCCLIP 9
:|||||
Db 161 YNNCCFFP 169
RESULT 30
AAY24163
ID AAY24163 standard; peptide; 16 AA.
XX AAY24163;
AC

10-SEP-1999 (first entry)

Alpha-conotoxin peptide SEQ ID NO:9.

Alpha-conotoxin; neuronal nicotinic acetylcholine receptor; nAChR; small cell lung carcinoma; cardiovascular disorder; nicotine addiction; gastric motility disorder; urinary incontinence; mood disorder; bipolar disorder; unipolar depression; dysthymia; seasonal affective disorder.

Conus purpurascens.

WO9933482-A1.

08-JUL-1999.

23-DEC-1998; 98WO-US027367.

31-DEC-1997; 97US-0070153P.

03-APR-1998; 98US-0060588P.

(UTAH) UNIV UTAH RES FOUND.

Olivera BM, McIntosh JM, Yoshikami D, Cartier GE, Luo S;

WPI; 1999-405367/34.

Alpha-conotoxin peptides that are used to treat disorders regulated at neuronal nicotinic acetylcholine receptors.

Claim 28; Page 6; 40pp; English.

The present sequence represents a specifically claimed example of an alpha-conotoxin, which can be used to treat disorders regulated at neuronal nicotinic acetylcholine receptors (nAChR). The alpha-conotoxins are useful for preparing a pharmaceutical composition for treating disorders regulated at neuronal nAChR, especially alpha 3 beta 2, alpha 3 beta 4 or alpha 7-containing nAChR. Disorders that can be treated include cardiovascular disorders, a gastric motility disorder, urinary incontinence, nicotine addiction, a mood disorder or small cell lung carcinoma. Mood disorders include bipolar disorder, unipolar depression, dysthymia and seasonal affective disorder. The alpha- conotoxins can also be used for diagnosis of small cell lung carcinoma. The alpha-conotoxin antagonists are able to discriminate between non- symmetrical ligand binding interfaces present on the nAChR. The alpha- conotoxin has the ability to potentially block any receptor containing a alpha beta subunit interface, regardless of what other subunits may be present in the receptor complex

Sequence 16 AA;

Query Match 39.0%; Score 48; DB 2; Length 16;
Best Local Similarity 40.0%; Pred. No. 17;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19.

2 CCSLPFCAANNPDYC 16

ULT 31

24887

AAW24887 standard; peptide; 18 AA.

AAW24887;

25-MAR-2003 (revised)

15-OCT-1997 (first entry)

Predatory cone snail venom alpha-conotoxin SL-1.

Conotoxin; venom; predatory; cone snail; Conus; A-lineage; inhibitor;

KW synaptic transmission; neuromuscular junction; block; alpha-conotoxin;
KW nicotinic acetylcholine receptor; kappa-conotoxin;
KW voltage-sensitive potassium CHANNEL; sodium channel.

OS Conus sulcatus.

XX Key Location/Qualifiers

XX Modified-site 7

FT /note= "optionally 4Hyp"

FT Modified-site 14

FT /note= "optionally 4Hyp"

FT Misc-difference 15

FT /label= Glu, OTHER

FT /note= "OTHER = gamma-carboxyglutamate (Glu)"

FT Modified-site 18

FT /note= "amidated C-terminus"

XX US5633347-A.

PN 27-MAY-1997.

XX 07-JUN-1995; 95US-00480750.

XX 29-JUN-1993; 93US-00084848.

PR 19-OCT-1993; 93US-00137800.

XX (UTAH) UNIV UTAH RES FOUND.

XX Hillyard DR, Cruz LJ, McIntosh JM, Santos AO, Olivera BM;

XX WPI; 1997-309336/28.

XX New kappa-conotoxin peptide(s) - present in venom of fish-hunting cone snail.

PS Disclosure; Col 5; 37pp; English.

CC The peptides AAW24878-W24900 represent novel toxin peptides isolated from the venom of various predatory cone snails of the genus Conus. The peptides are A-lineage conotoxin peptides which fall into 3 groups dependent on their amino acid sequences: (i) alpha-3/5 have a core sequence CCXXCXKXXXC where X is any amino acid; (ii) alpha-4/7 have a core sequence CCXXCXKXXXC; and (iii) kappa-7/2/1/3 have the core sequence CCXXXXXXCXKXXXC. The peptide presented here was isolated from Conus sulcatus and falls into the alpha-4/7 category. Alpha-conotoxin peptides are potent inhibitors of synaptic transmission at the neuromuscular junction by blocking nicotinic acetylcholine receptors, whereas kappa-conotoxins have activities against voltage-sensitive potassium or sodium channels. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 18 AA;

Query Match 39.0%; Score 48; DB 2; Length 18;
Best Local Similarity 46.7%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 5 CCLIPACRRNHKKFC 19

Db 3 CCSFPACRKYPXMC 17

RESULT 32

AAW24887

ID AAW24887 standard; peptide; 18 AA.

XX AAW24887;

XX 18-JUL-2000 (first entry)

XX Mature conotoxin peptide #2.

XX Mature conotoxin; brocade cone shell; line cone shell; drug screening;

neuronal inhibitor; muscle inhibitor.

Conus sp.

CN1237584-A.

08-DEC-1999.

30-APR-1999; 99CN-00106070.

30-APR-1999; 99CN-00106070.

(BIOL-) BIOLOGICAL ENG INST ACAD MILITARY MEDICI.

Lu B, Huang P;

WPI; 2000-351193/31.

Conotoxin peptide from brocade, cone shells useful as analgesic.

Claim 1A; Page 2; 20pp; Chinese.

The invention relates to 14 novel mature conotoxin peptides from marine snails (Conus species); conotoxin precursor proteins; and cDNAs encoding the conotoxin precursors. The mature peptide sequences were discovered by obtaining conotoxin cDNA sequences from mRNA from the brocade cone shell (Conus textile) or the line cone shell (Conus striatus). The cDNA sequences were used to determine the conotoxin precursor protein sequences, and the sequences of the mature conotoxin peptides were inferred from the precursor sequences. The mature conotoxin peptides can be obtained via chemical synthesis or by in vitro gene expression. Conotoxins inhibit the function of neurons and muscle cells. Certain conotoxins interfere with synaptic transmission, while others act on muscle or at the neuromuscular junction. The 14 novel conotoxins have unique receptor specificity and affinity, so can be used as screening tools to identify new drugs. Conotoxin #11 (AAV87540) may be used for pain relief. Sequences AAV87420, AAV87524, AAV87526, AAV87528, AAV87530, AAV87532, AAV87534, AAV87536, AAV87538, AAV87540, AAV87542, AAV87544 and AAV87546 represent mature conotoxins #1-#14, respectively

Sequence 18 AA;

Query Match 39.0%; Score 48; DB 3; Length 18;
Best Local Similarity 46.7%; Pred. No. 19;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19
||| : : :
3 CASHPACNVDPHEIC 17

MULT 33

321523

AAV87523 standard; peptide; 18 AA.

AAV87523;

22-JAN-2001 (first entry)

Cone snail alpha-conotoxin SEQ ID NO: 203.

Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
neuronal nicotinic acetylcholine receptor; cardiovascular disorder;
gastric motility disorder; urinary incontinence; nicotine addiction;
small cell lung carcinoma.

Conus musicus.

Key Location/Qualifiers

Misc-difference 2

/label= Lys, OTHER
/note= "N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys"

FT Misc-difference 12
FT /label= Lys, OTHER
FT /note= "N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys"

FT Misc-difference 14

FT /label= Pro, OTHER
FT /note= "hydroxy-Pro"

FT Misc-difference 16

FT /label= Tyr, OTHER
FT /note= "mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr"

XX WO200044776-A1.

XX 03-AUG-2000.

XX 28-JAN-2000; 2000WO-US001979.

XX 29-JAN-1999; 99US-0118381P.

XX (UTAH) UNIV UTAH RES FOUND.

XX (COGN-) COGNETIX INC.

XX Watkins M, Oliveira BM, Hillyard DR, McIntosh JM, Jones RM;

XX WPI; 2000-505965/45.

XX alpha-conotoxin polypeptides derived from the venom of cone snails useful e.g. as neuromuscular blocking agents for use in surgery and for treating unipolar depression.

XX Claim 21, Page 80; 229pp; English.

XX The present invention relates to a number of alpha-conotoxin peptides and their coding sequences from a number of different species of cone snail. These peptides are found in minute quantities in the venom of the snails, and are targeted at the neuronal nicotinic acetylcholine receptors of the nervous system. They usually contain two disulphide bonds, which give them defined conformations, a rarity in molecules this small. The alpha-conotoxins can be used as neuromuscular blocking agents in surgery, and for treating disorders regulated at the neuronal nicotinic acetylcholine receptors, including cardiovascular disorders, gastric motility disorders, urinary incontinence, nicotine addiction, mood disorders such as bipolar disorder, unipolar depression, dysthymia and seasonal affective disorder, and small cell lung carcinoma

XX Sequence 18 AA;

Query Match 39.0%; Score 48; DB 3; Length 18;
Best Local Similarity 46.7%; Pred. No. 19;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 5 CCLIPACRRNHKKFC 19

||| : : :
3 CCINDACRSXHXQC 17

RESULT 34

AAV87523

ID AAV87523 standard; peptide; 18 AA.

XX AAV87523;

XX 19-JAN-2001 (first entry)

XX Cone snail alpha-conotoxin SEQ ID NO: 396.

XX Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
neuronal nicotinic acetylcholine receptor; cardiovascular disorder;
gastric motility disorder; urinary incontinence; nicotine addiction;
small cell lung carcinoma.

XX Conus textile.

WO200044776-A1.

03-AUG-2000.

28-JAN-2000; 2000WO-US001979.

29-JAN-1999; 99US-0118381P.

(UTAH) UNIV UTAH RES FOUND.
(COGN-) COGNETIX INC.

Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

WPI; 2000-505965/45.
N-PSDB; AAA89530.

alpha-conotoxin polypeptides derived from the venom of cone snails useful
e.g. as neuromuscular blocking agents for use in surgery and for treating
unipolar depression.

Claim 39; Page 65; 229pp; English.

The present invention relates to a number of alpha-conotoxin peptides and
their coding sequences from a number of different species of cone snail.
These peptides are found in minute quantities in the venom of the snails,
and are targeted at the neuronal nicotinic acetylcholine receptors of the
nervous system. They usually contain two disulphide bonds, which give
them defined conformations, a rarity in molecules this small. The alpha-
conotoxins can be used as neuromuscular blocking agents in surgery, and
for treating disorders regulated at the neuronal nicotinic acetylcholine
receptors, including cardiovascular disorders, gastric motility
disorders, urinary incontinence, nicotine addiction, mood disorders such
as bipolar disorder, unipolar depression, dysthymia and seasonal
affective disorder, and small cell lung carcinoma

Sequence 38 AA;

Query Match 39.0%; Score 48; DB 3; Length 38;
est Local Similarity 46.7%; Pred. No. 36;
atches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHHKFC 19
||| : : :
23 CCSHPACNVDPHC 37

ULT 35
21586

AAB21586 standard; peptide; 39 AA.

AAB21586;

19-JAN-2001 (first entry)

Cone snail alpha-conotoxin SEQ ID NO: 300.

Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
neuronal nicotinic acetylcholine receptor; cardiovascular disorder;
gastric motility disorder; urinary incontinence; nicotine addiction;
small cell lung carcinoma.

Conus arenatus.

WO200044776-A1.

03-AUG-2000.

28-JAN-2000; 2000WO-US001979.

29-JAN-1999; 99US-0118381P.

(UTAH) UNIV UTAH RES FOUND.

PA (COGN-) COGNETIX INC.

XX Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

XX WPI; 2000-505965/45.

XX N-PSDB; AAA89482.

XX alpha-conotoxin polypeptides derived from the venom of cone snails useful
e.g. as neuromuscular blocking agents for use in surgery and for treating
unipolar depression.

XX Claim 39; Page 54; 229pp; English.

XX The present invention relates to a number of alpha-conotoxin peptides and
their coding sequences from a number of different species of cone snail.
These peptides are found in minute quantities in the venom of the snails,
and are targeted at the neuronal nicotinic acetylcholine receptors of the
nervous system. They usually contain two disulphide bonds, which give
them defined conformations, a rarity in molecules this small. The alpha-
conotoxins can be used as neuromuscular blocking agents in surgery, and
for treating disorders regulated at the neuronal nicotinic acetylcholine
receptors, including cardiovascular disorders, gastric motility
disorders, urinary incontinence, nicotine addiction, mood disorders such
as bipolar disorder, unipolar depression, dysthymia and seasonal
affective disorder, and small cell lung carcinoma

SQ Sequence 39 AA;

Query Match 39.0%; Score 48; DB 3; Length 39;
Best Local Similarity 53.3%; Pred. No. 37;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHHKFC 19

||| : : :
22 CCSNPACRVNPHVC 36

Search completed: February 18, 2004, 06:06:09

Job time : 97 secs

GenCore version 5.1.6
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protein - protein search, using sw model

on: February 18, 2004, 06:07:14 ; Search time 608 Seconds

(without alignments)
6.599 Million cell updates/sec

le: US-09-806-376-1

fect score: 123

uence: 1 FNRCCLPACRRNHKKFC 19

ring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

rchd: 809742 seqs, 211153259 residues

al number of hits satisfying chosen parameters: 809742

imum DB seq length: 0

imum DB seq length: 2000000000

t-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

abase : Published Applications AA:

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pcp.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pcp.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pcp.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pcp.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pcp.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pcp.*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pcp.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pcp.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pcp.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Match	Length	DB	ID	Description
1	50	40.7	76	10	US-09-910-009A-189	Sequence 189, App
2	49.5	40.2	25	15	US-10-430-545-2	Sequence 2, Appli
3	49	39.8	17	14	US-10-072-602B-605	Sequence 605, App
4	49	39.8	60	14	US-10-072-602B-409	Sequence 409, App
5	48	39.0	16	9	US-09-897-465-9	Sequence 9, Appli
6	48	39.0	64	14	US-10-050-704-154	Sequence 154, App
7	48	39.0	76	9	US-09-768-847-511	Sequence 511, App
8	48	39.0	76	14	US-10-092-154-511	Sequence 511, App
9	48	39.0	150	9	US-09-915-582-63	Sequence 63, Appl
10	48	39.0	150	9	US-09-915-582-83	Sequence 83, Appl
11	48	39.0	150	10	US-09-832-129-49	Sequence 49, Appl
12	48	39.0	150	11	US-09-833-245-1472	Sequence 1472, Ap
13	48	39.0	150	11	US-09-833-245-1473	Sequence 1473, Ap
14	48	39.0	150	11	US-09-833-245-2227	Sequence 2227, Ap
15	48	39.0	150	14	US-10-050-704-182	Sequence 182, App

Sequence 63, Appl
Sequence 83, Appl
Sequence 61, Appl
Sequence 158, App
Sequence 601, App
Sequence 774, App
Sequence 1202, Ap
Sequence 981, App
Sequence 10, Appl
Sequence 598, App
Sequence 599, App
Sequence 392, App
Sequence 395, App
Sequence 111, App
Sequence 2498, Ap
Sequence 152, App
Sequence 152, App
Sequence 428, App
Sequence 89, Appl
Sequence 349, App
Sequence 568, App
Sequence 608, App
Sequence 220, App
Sequence 278, App
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 6, Appli
Sequence 17, Appl
Sequence 1416, Ap
Sequence 39, Appl
Sequence 2, Appli
Sequence 612, App

ALIGNMENTS

RESULT 1

US-09-910-009A-189
; Sequence 189, Application US/09910009A
; Publication No. US20030050234A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; APPLICANT: Shen, Greg S.
; APPLICANT: Megstaff, John D.
; TITLE OF INVENTION: Mu-Conopeptides
; FILE REFERENCE: 2314-242
; CURRENT APPLICATION NUMBER: US/09/910,009A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,619
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/245,157
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/264,319
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: US 60/277,270
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 520
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 189

LENGTH: 76
 TYPE: PRT
 ORGANISM: Conus radiatus
 09-910-009A-189

Query Match 40.7%; Score 50; DB 10; Length 76;
 Best Local Similarity 61.5%; Pred. No. 14;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

2 NRCLIPACRN 14
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 59 NRCLIPACRN 71
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ULT 2
 10-430-545-2
 Sequence 2, Application US/10430545
 Publication No. US20040014660A1
 GENERAL INFORMATION:
 APPLICANT: Daring, Matthew
 APPLICANT: Collin, Haile
 TITLE OF INVENTION: Insulin-Associated Peptides With Effects On Cerebral Health
 FILE REFERENCE: 102182-34
 CURRENT APPLICATION NUMBER: US/10/430,545
 PRIOR FILING DATE: 2003-05-06
 PRIOR APPLICATION NUMBER: 60/378,318
 PRIOR FILING DATE: 2002-05-06
 NUMBER OF SEQ ID NOS: 3
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 2
 LENGTH: 25
 TYPE: PRT
 ORGANISM: Homo sapiens
 10-430-545-2

Query Match 40.2%; Score 49.5; DB 15; Length 25;
 Best Local Similarity 52.9%; Pred. No. 6.5;
 Matches 9; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

4 RCLIPAC-RRNHKFC 19
 |||||:
 9 KCCLGACTKRSKAYC 25
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 |||||:

SULT 3
 10-072-602B-605
 Sequence 605, Application US/10072602B
 Publication No. US20030109670A1
 GENERAL INFORMATION:
 APPLICANT: University of Utah Research Foundation
 APPLICANT: Cognetix, Inc.
 APPLICANT: Olivera, Baldomero M.
 APPLICANT: McIntosh, J. Michael
 APPLICANT: Watkins, Maren
 APPLICANT: Garrett, James E.
 APPLICANT: Cruz, Lourdes J.
 APPLICANT: Grille, Michelle
 APPLICANT: Schoenfeld, Robert M.
 APPLICANT: Walker, Craig
 APPLICANT: Shetty, Reshma
 APPLICANT: Jones, Robert M.
 TITLE OF INVENTION: Cone Snail Peptides
 FILE REFERENCE: 2314-249
 CURRENT APPLICATION NUMBER: US/10/072,602B
 PRIOR FILING DATE: 2002-02-11
 PRIOR APPLICATION NUMBER: US 60/267,408
 PRIOR FILING DATE: 2001-02-09
 NUMBER OF SEQ ID NOS: 638
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 605
 LENGTH: 17
 TYPE: PRT
 ORGANISM: Conus bandanus

US-10-072-602B-605
 Query Match 39.8%; Score 49; DB 14; Length 17;
 Best Local Similarity 46.7%; Pred. No. 5.5;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKFC 19
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 Db 3 CCHPACHVSHPELC 17
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RESULT 4
 US-10-072-602B-409
 Sequence 409, Application US/10072602B
 Publication No. US20030109670A1
 GENERAL INFORMATION:
 APPLICANT: University of Utah Research Foundation
 APPLICANT: Cognetix, Inc.
 APPLICANT: Olivera, Baldomero M.
 APPLICANT: McIntosh, J. Michael
 APPLICANT: Watkins, Maren
 APPLICANT: Garrett, James E.
 APPLICANT: Cruz, Lourdes J.
 APPLICANT: Grille, Michelle
 APPLICANT: Schoenfeld, Robert M.
 APPLICANT: Walker, Craig
 APPLICANT: Shetty, Reshma
 APPLICANT: Jones, Robert M.
 TITLE OF INVENTION: Cone Snail Peptides
 FILE REFERENCE: 2314-249
 CURRENT APPLICATION NUMBER: US/10/072,602B
 PRIOR FILING DATE: 2002-02-11
 PRIOR APPLICATION NUMBER: US 60/267,408
 PRIOR FILING DATE: 2001-02-09
 NUMBER OF SEQ ID NOS: 638
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 409
 LENGTH: 60
 TYPE: PRT
 ORGANISM: Conus bandanus
 US-10-072-602B-409

Query Match 39.8%; Score 49; DB 14; Length 60;
 Best Local Similarity 46.7%; Pred. No. 16;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKFC 19
 |||||:
 Db 45 CCHPACHVSHPELC 59
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RESULT 5
 US-09-897-465-9
 Sequence 9, Application US/09897465
 Patent No. US20020022715A1
 GENERAL INFORMATION:
 APPLICANT: Olivera, Baldomero M.
 APPLICANT: McIntosh, J. Michael
 APPLICANT: Yoshikami, Doju
 APPLICANT: Cartier, G. Edward
 APPLICANT: Luo, Siqin
 APPLICANT: University of Utah Research Foundation
 TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
 FILE REFERENCE: Uses of Alpha-Conotoxins
 CURRENT APPLICATION NUMBER: US/09/897,465
 CURRENT FILING DATE: 2001-07-03
 PRIOR APPLICATION NUMBER: US 60/080,588
 PRIOR FILING DATE: 1998-04-03
 PRIOR APPLICATION NUMBER: US 60/070,153
 PRIOR FILING DATE: 1997-12-31
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 9

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LENGTH: 16
TYPE: EXT
ORGANISM: Conus purpurascens
9-897-465-9
    39.0%; Score 48; DB 9; Length 16;
    1st Local Similarity 40.0%; Pred. No. 7.1;
    tches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19
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2 CCLIPCAANPDYC 16

LT 6
0-050-704-154
quence 154, Application US/10050704
blication No. US20030050442A1
NERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 62 Human Secreted Proteins
FILE REFERENCE: P203921
CURRENT APPLICATION NUMBER: US/10/050,704
CURRENT FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: 09/684,524
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: PCT/US00/08979
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/128,693
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: 60/130,991
PRIOR FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 344
SOFTWARE: PatentIn Ver. 2.0
Q ID NO 154
LENGTH: 64
TYPE: EXT
ORGANISM: Homo sapiens
0-050-704-154
    39.0%; Score 48; DB 14; Length 64;
    1st Local Similarity 75.0%; Pred. No. 23;
    tches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

2 NWRCCLIP 9
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39 NWKCCFIP 46

LT 7
9-764-847-511
quence 511, Application US/09764847
tent No. US20020132767A1
NERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 2003
SOFTWARE: PatentIn Ver. 2.0
Q ID NO 511
LENGTH: 76
TYPE: EXT
ORGANISM: Homo sapiens
9-764-847-511
    39.0%; Score 48; DB 9; Length 76;
    1st Local Similarity 53.8%; Pred. No. 26;
    tches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

7 LIPACRRNHKKFC 19

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Db          60 IVPKCRPHKEGC 72
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RESULT 8
US-10-092-154-511
; Sequence 511, Application US/10092154
; Publication No. US20030054375A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009C1
; CURRENT APPLICATION NUMBER: US/10/092,154
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2003
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 511
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-154-511
Query Match          39.0%; Score 48; DB 14; Length 76;
Best Local Similarity 53.8%; Pred. No. 26;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY          7 LIPACRNHKKFC 19
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Db          60 IVPKCRPHKEGC 72
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RESULT 9
US-09-915-582-63
; Sequence 83, Application US/09915582
; Patent No. US20020120103A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 17 Human Secreted Proteins
; FILE REFERENCE: PS723P1
; CURRENT APPLICATION NUMBER: US/09/915,582
; CURRENT FILING DATE: 2001-07-27
; Prior Application Number: PCT/US01/01431
; Prior Filing Date: 2001-01-17
; Prior Application Number: 60/179,065
; Prior Filing Date: 2000-01-31
; Prior Application Number: 60/180,628
; Prior Filing Date: 2000-02-04
; Prior Application Number: 60/231,968
; Prior Filing Date: 2000-09-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-582-63
Query Match          39.0%; Score 48; DB 9; Length 150;
Best Local Similarity 75.0%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY          2 NWRCCLIP 9
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Db          125 NWKCCFIP 132
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RESULT 10
US-09-915-582-83
; Sequence 83, Application US/09915582
; Patent No. US20020120103A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

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TITLE OF INVENTION: 17 Human Secreted Proteins
FILE REFERENCE: PS723PI
CURRENT APPLICATION NUMBER: US/09/915,582
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: PCT/US01/01431
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/231,968
PRIOR FILING DATE: 2000-09-12
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 83
LENGTH: 150
TYPE: PRT
ORGANISM: Homo sapiens
J9-915-582-83

Query Match 39.0%; Score 48; DB 9; Length 150;
Best Local Similarity 75.0%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 2 NWRCCCLIP 9
DB 125 NWKCCFIP 132

RESULT 11
US-09-832-129-49
Sequence 49, Application US/09832129
Publication No. US20030027297A1
GENERAL INFORMATION:
APPLICANT: Fiscella et al.
TITLE OF INVENTION: 19 Human secreted proteins
FILE REFERENCE: P2045P1
CURRENT APPLICATION NUMBER: US/09/832,129
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: PCT/US00/28664
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/163,085
PRIOR FILING DATE: 1999-11-02
PRIOR APPLICATION NUMBER: 60/172,411
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.0
EQ ID NO 49
LENGTH: 150
TYPE: PRT
ORGANISM: Homo sapiens
09-832-129-49

Query Match 39.0%; Score 48; DB 10; Length 150;
Best Local Similarity 75.0%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 2 NWRCCCLIP 9
DB 125 NWKCCFIP 132

RESULT 12
US-833-245-1472
Sequence 1472, Application US/09833245
Publication No. US20040010134A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256,931
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199,384
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PatentIn Ver. 2.1

TITLE OF INVENTION: 17 Human Secreted Proteins
FILE REFERENCE: PS723PI
CURRENT APPLICATION NUMBER: US/09/915,582
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: PCT/US01/01431
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/231,968
PRIOR FILING DATE: 2000-09-12
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 83
LENGTH: 150
TYPE: PRT
ORGANISM: Homo sapiens
US-09-833-245-1472

Query Match 39.0%; Score 48; DB 11; Length 150;
Best Local Similarity 75.0%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 2 NWRCCCLIP 9
DB 125 NWKCCFIP 132

RESULT 13
US-09-833-245-1473
Sequence 1473, Application US/09833245
Publication No. US20040010134A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256,931
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199,384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1473
LENGTH: 150
TYPE: PRT
ORGANISM: Homo sapiens
US-09-833-245-1473

Query Match 39.0%; Score 48; DB 11; Length 150;
Best Local Similarity 75.0%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 2 NWRCCCLIP 9
DB 125 NWKCCFIP 132

RESULT 14
US-09-833-245-2227
Sequence 2227, Application US/09833245
Publication No. US20040010134A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256,931
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199,384
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PatentIn Ver. 2.1

3Q ID NO 2227
LENGTH: 150
TYPE: PRT
ORGANISM: Homo sapiens
J9-833-245-2227

Query Match 39.0%; Score 48; DB 11; Length 150;
Best Local Similarity 75.0%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

2 NWRCCCLIP 9
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125 NWKCCFIP 132

ULT 15
10-050-704-182
Sequence 83, Application US/10050704
Publication No. US20030050442A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 62 Human Secreted Proteins
FILE REFERENCE: P2039P1
CURRENT APPLICATION NUMBER: US/10/050,704
CURRENT FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: 09/684,524
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: PCT/US00/08979
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/128,693
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: 60/130,991
PRIOR FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 344
SOFTWARE: PatentIn Ver. 2.0
EQ ID NO 182
LENGTH: 150
TYPE: PRT
ORGANISM: Homo sapiens
10-050-704-182

Query Match 39.0%; Score 48; DB 14; Length 150;
Best Local Similarity 75.0%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

2 NWRCCCLIP 9
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125 NWKCCFIP 132

ULT 16
10-277-802-63
Sequence 63, Application US/10277802
Publication No. US20030190707A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 17 Human Secreted Proteins
FILE REFERENCE: PS723P1
CURRENT APPLICATION NUMBER: US/10/277,802
CURRENT FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: 09/915,582
PRIOR FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: PCT/US01/01431
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/231,968
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn Ver. 2.0
EQ ID NO 63

3Q ID NO 2227
LENGTH: 150
TYPE: PRT
ORGANISM: Homo sapiens
US-10-277-802-63

Query Match 39.0%; Score 48; DB 14; Length 150;
Best Local Similarity 75.0%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

2 NWRCCCLIP 9
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125 NWKCCFIP 132

RESULT 17
US-10-277-802-83
Sequence 83, Application US/10277802
Publication No. US20030190707A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 17 Human Secreted Proteins
FILE REFERENCE: PS723P1
CURRENT APPLICATION NUMBER: US/10/277,802
CURRENT FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: 09/915,582
PRIOR FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: PCT/US01/01431
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/231,968
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 83
LENGTH: 150
TYPE: PRT
ORGANISM: Homo sapiens
US-10-277-802-83

Query Match 39.0%; Score 48; DB 14; Length 150;
Best Local Similarity 75.0%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

2 NWRCCCLIP 9
||:||||
125 NWKCCFIP 132

RESULT 18
US-09-832-129-64
Sequence 64, Application US/09832129
Publication No. US20030027297A1
GENERAL INFORMATION:
APPLICANT: Fiscella et al.
TITLE OF INVENTION: 19 Human secreted proteins
FILE REFERENCE: P2045P1
CURRENT APPLICATION NUMBER: US/09/832,129
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: PCT/US00/28664
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/163,085
PRIOR FILING DATE: 1999-11-02
PRIOR APPLICATION NUMBER: 60/172,411
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 64
LENGTH: 192
TYPE: PRT
ORGANISM: Homo sapiens

09-832-129-64
Query Match 39.0%; Score 48; DB 10; Length 192;
Best Local Similarity 75.0%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

2 NWRCClip 9
||:||||
167 NWKCCFIP 174

ULT 19
10-205-823-158
Sequence 158, Application US/10205823
Publication No. US20030108963A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Endege, Wilson O.
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gorbatscheva, Bella
APPLICANT: Hoersch, Sebastian
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Womsey, Angela M.
APPLICANT: Glatt, Karen
APPLICANT: Zhao, Xumei
APPLICANT: Anderson, Dustin
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
THERAPY OF PROSTATE CANCER
FILE REFERENCE: WRI-044
CURRENT APPLICATION NUMBER: US/10/205,823
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,982
PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 158
LENGTH: 338
TYPE: PRT
ORGANISM: Homo sapiens
10-205-823-158

Query Match 39.0%; Score 48; DB 14; Length 338;
Best Local Similarity 75.0%; Pred. No. 90;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

2 NWRCClip 9
||:||||
313 NWKCCFIP 320

ULT 20
10-225-567A-601
Sequence 601, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burner, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 601
LENGTH: 338
TYPE: PRT
ORGANISM: Homo sapiens
US-10-225-567A-601

Query Match 39.0%; Score 48; DB 14; Length 338;
Best Local Similarity 75.0%; Pred. No. 90;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NWRCClip 9
||:||||
Db 313 NWKCCFIP 320

RESULT 21
US-10-295-027-774
Sequence 774, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynn, Richard
APPLICANT: Hevizi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 774
LENGTH: 338
TYPE: PRT
ORGANISM: Homo sapiens
US-10-295-027-774

Query Match 39.0%; Score 48; DB 15; Length 338;
Best Local Similarity 75.0%; Pred. No. 90;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NWRCClip 9

313 NWKCCFIP 320

UT 22

10-295-027-1202
 sequence 1202, Application US/10295027
 Publication No. US20030232350A1
 GENERAL INFORMATION:
 APPLICANT: Afar, Daniel
 APPLICANT: Aziz, Nataasha
 APPLICANT: Ginsberg, Wendy M.
 APPLICANT: Gish, Kurt C.
 APPLICANT: Glynn, Richard
 APPLICANT: Hevezi, Peter A.
 APPLICANT: Mack, David H.
 APPLICANT: Murray, Richard
 APPLICANT: Watson, Susan R.
 APPLICANT: Eos Biotechnology, Inc.

TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
 TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
 FILE REFERENCE: 018501-012500US
 CURRENT APPLICATION NUMBER: US/10/295,027
 CURRENT FILING DATE: 2002-11-13

PRIOR APPLICATION NUMBER: US 09/663,733
 PRIOR FILING DATE: 2000-09-15
 PRIOR APPLICATION NUMBER: US 60/350,666
 PRIOR FILING DATE: 2001-11-13
 PRIOR APPLICATION NUMBER: US 60/335,394
 PRIOR FILING DATE: 2001-11-15
 PRIOR APPLICATION NUMBER: US 60/332,464
 PRIOR FILING DATE: 2001-11-21
 PRIOR APPLICATION NUMBER: US 60/334,393
 PRIOR FILING DATE: 2001-11-29
 PRIOR APPLICATION NUMBER: US 60/340,376
 PRIOR FILING DATE: 2001-12-14
 PRIOR APPLICATION NUMBER: US 60/347,211
 PRIOR FILING DATE: 2002-01-08
 PRIOR APPLICATION NUMBER: US 60/347,349
 PRIOR FILING DATE: 2002-01-10
 PRIOR APPLICATION NUMBER: US 60/355,250
 PRIOR FILING DATE: 2002-02-08
 PRIOR APPLICATION NUMBER: US 60/356,714
 PRIOR FILING DATE: 2002-02-13
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 1386
 SOFTWARE: PatentIn Ver. 2.1
 EQ ID NO 1202
 LENGTH: 338
 TYPE: PRT
 ORGANISM: Homo sapiens
 10-295-027-1202

Query Match 39.0%; Score 48; DB 15; Length 338;
 Best Local Similarity 75.0%; Pred. No. 90;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

2 NWKCCFIP 9
 313 NWKCCFIP 320

UT 23

09-923-301-981
 sequence 981, Application US/09925301
 Patent No. US2002052308A1
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 FILE REFERENCE: P106
 CURRENT APPLICATION NUMBER: US/09/925,301
 CURRENT FILING DATE: 2001-08-10
 PRIOR APPLICATION NUMBER: PCT/US00/05882

PRIOR FILING DATE: 2000-03-08
 PRIOR APPLICATION NUMBER: 60/124,270
 PRIOR FILING DATE: 1999-03-12
 NUMBER OF SEQ ID NOS: 1694
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 981
 LENGTH: 343
 TYPE: PRT
 ORGANISM: Homo sapiens
 NAME/KEY: SITE
 LOCATION: (343)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 US-09-925-301-981

Query Match 39.0%; Score 48; DB 9; Length 343;
 Best Local Similarity 75.0%; Pred. No. 91;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 NWKCCFIP 9
 Db 318 NWKCCFIP 325

RESULT 24

US-09-897-465-10
 Sequence 10, Application US/09897465
 Patent No. US2002022715A1
 GENERAL INFORMATION:
 APPLICANT: Oliveira, Baldozero M.
 APPLICANT: McIntosh, J. Michael
 APPLICANT: Yoshikami, Doju
 APPLICANT: Cartier, G. Edward
 APPLICANT: Luo, Siqin
 APPLICANT: University of Utah Research Foundation
 TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
 FILE REFERENCE: Uses of Alpha-Conotoxins
 CURRENT APPLICATION NUMBER: US/09/897,465
 CURRENT FILING DATE: 2001-07-03
 PRIOR APPLICATION NUMBER: US 60/080,588
 PRIOR FILING DATE: 1998-04-03
 PRIOR APPLICATION NUMBER: US 60/070,153
 PRIOR FILING DATE: 1997-12-31
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: PatentIn Ver. 2.0
 EQ ID NO 10
 LENGTH: 16
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: A10L derivative
 OTHER INFORMATION: of C. purpurascens PnIA
 US-09-897-465-10

Query Match 38.2%; Score 47; DB 9; Length 16;
 Best Local Similarity 40.0%; Pred. No. 9.7;
 Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 5 CCLIPACRRNHKKFC 19
 Db 2 CCSLPPCALNNDYC 16

RESULT 25

US-10-072-602B-598
 Sequence 598, Application US/10072602B
 Publication No. US20030109670A1
 GENERAL INFORMATION:
 APPLICANT: University of Utah Research Foundation
 APPLICANT: Cognetix, Inc.
 APPLICANT: Oliveira, Baldozero M.
 APPLICANT: McIntosh, J. Michael
 APPLICANT: Watkins, Maren

|||||:|:|:|
45 OCTIPSCWDYKERC 59

LT 29
0-097-340-111
Sequence 111, Application US/10097340
Publication No. US20030087250A1

GENERAL INFORMATION:
APPLICANT: John MONAHAN

APPLICANT: Manjula GANNAVAPU

APPLICANT: Sebastian HOERSCH

APPLICANT: Shubhangi KAMATKAR

APPLICANT: Steve G. KOVATS

APPLICANT: Rachel E. MEYERS

APPLICANT: Michael MORRISSEY

APPLICANT: Peter OLANDT

APPLICANT: Ami SEN

APPLICANT: Peter VEIBY

APPLICANT: Gordon B. MILLS

APPLICANT: Robert C. BAST, Jr.

APPLICANT: Karen LU

APPLICANT: Rosemarie SCHMANDT

APPLICANT: Xumei ZHAO

APPLICANT: Karen GLATT

TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,

FILE REFERENCE: MRI-030

CURRENT APPLICATION NUMBER: US/10/097,340

PRIOR FILING DATE: 2002-03-14

PRIOR APPLICATION NUMBER: 60/276,025

PRIOR FILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: 60/325,149

PRIOR FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 60/276,026

PRIOR FILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: 60/324,967

PRIOR FILING DATE: 2001/09/26

PRIOR APPLICATION NUMBER: 60/311,732

PRIOR FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: 60/325,102

PRIOR FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 60/323,580

PRIOR FILING DATE: 2001-09-19

NUMBER OF SEQ ID NOS: 363

SOFTWARE: Fast-SEQ for Windows Version 4.0

SEQ ID NO 111

LENGTH: 257

TYPE: PRT

ORGANISM: Homo sapiens

10-097-340-111

Query Match 38.2%; Score 47; DB 14; Length 257;

Best Local Similarity 50.0%; Pred. No. 97;

Matches 8; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

1 FNRCC--LIPACRN 14

|||||:|:|:|

84 FNNHCGEMAPACKRH 99

ULT 30

Sequence 2498, Application US/10264049

Publication No. US20040005579A1

GENERAL INFORMATION:

APPLICANT: Birse et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PA133P1

CURRENT APPLICATION NUMBER: US/10/264,049

CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: PCT/US01/18569

PRIOR FILING DATE: 2001-06-07

; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2498
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-2498

Query Match 38.2%; Score 47; DB 15; Length 270;
Best Local Similarity 50.0%; Pred. No. 1e+02; 3; Indels 2; Gaps 1;
Matches 8; Conservative 3; Mismatches 3; Indels 2; Gaps 1;
QY 1 FNRCC--LIPACRN 14
|||||:|:|:|
DB 97 FNNHCGEMAPACKRH 112

RESULT 31
US-09-205-658-152
; Sequence 152, Application US/09205658
; Patent No. US20010029617A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 152
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(46)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-205-658-152

Query Match 37.4%; Score 46; DB 9; Length 46;
Best Local Similarity 43.8%; Pred. No. 32;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 4 RCCLIPACRNHHKFC 19
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DB 31 KCCLIGCTKRSKAYC 46

RESULT 32
US-09-963-693-152
; Sequence 152, Application US/09963693
; Publication No. US20030181364A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/963,693
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/205,658
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 08/857,076

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PRIORITY FILING DATE: 1997-05-15
PRIORITY APPLICATION NUMBER: 08/888,534
PRIORITY FILING DATE: 1997-07-07
PRIORITY APPLICATION NUMBER: US98/10080
PRIORITY FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 328
SOFTWARE: FASTSEQ for Windows Version 4.0
3Q ID NO 152
LENGTH: 46
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(46)
OTHER INFORMATION: Xaa = Any Amino Acid
J9-963-693-152

          37.4%;      Score 46;
          43.8%;      Pred. No.
          7;      Conservative
          4;      Mismatch

          4      RCLLIPACRRNHKKFC 19
          :|||:|:|
          31      KCLLIIGTCKSLAKYC 46

```

JLT 33
10-072-602B-428
sequence 428, Application US/10072602B
publication No. US20030109670A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation

APPLICANT: Cognetix, Inc.
 APPLICANT: Oliveta, Baldomero M.
 APPLICANT: McIntosh, J. Michael
 APPLICANT: Watkins, Maren E.
 APPLICANT: Garrett, James E.
 APPLICANT: Cruz, Lourdes J.
 APPLICANT: Grilley, Michelle
 APPLICANT: Schoenfeld, Robert M.
 APPLICANT: Walker, Craig
 APPLICANT: Shetty, Reshma
 APPLICANT: Jones, Robert M.
 TITLE OF INVENTION: Cone Snail Peptides
 FILE REFERENCE: 2314-249
 CURRENT APPLICATION NUMBER: US/10/072.602B
 CURRENT FILING DATE: 2002-02-11
 PRIOR APPLICATION NUMBER: P01/267,408
 PRIOR FILING DATE: 2001-02-09
 NUMBER OF SEQ ID NOS: 638
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 428
 LENGTH: 57

```

TYPE: PRT
ORGANISM: Conus leopardus
10-072-602B-428

luery Match 37.4%; Score 46; DB 14;
nest Local Similarity 43.8%; Pred. No. 38;
atches 7; Conservative 2; Mismatches 7

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4  RCCLIPACRRNHKKFC 19
   :|:|:|:|:|:|:|
41 KCCSNPACRRYNPAIC 56

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RESULT 34
 -09-908-741-89
 Sequence 89, Application US/09908741
 Publication No. US20030050435A1
 GENERAL INFORMATION:
 APPLICANT: Olivera, Baldomero M.
 APPLICANT: Laver, Richard T.

```

/ APPLICANT: Watkins, Maren
/ APPLICANT: Hillyard, David R.
/ APPLICANT: McIntosh, J. Michael
/ APPLICANT: Schoenfeld, Robert
/ APPLICANT: Jones, Robert M.
/ APPLICANT: Nielsen, Jake
/ APPLICANT: University of Utah Research Foundation
/ APPLICANT: Cognetix, Inc.
/ TITLE OF INVENTION: Alpha Conotoxin Peptides
/ FILE REFERENCE: Alpha CIP
/ CURRENT APPLICATION NUMBER: US/09/908,741
/ CURRENT FILING DATE: 2001-07-20
/ PRIOR APPLICATION NUMBER: US 60/116,881
/ PRIOR FILING DATE: 1999-01-22
/ PRIOR APPLICATION NUMBER: US 60/116,882
/ PRIOR FILING DATE: 1999-01-22
/ PRIOR APPLICATION NUMBER: US 09/488,799
/ PRIOR FILING DATE: 2000-01-21
/ PRIOR APPLICATION NUMBER: US 60/219,407
/ PRIOR FILING DATE: 2000-07-20
/ PRIOR APPLICATION NUMBER: US 60/221,557
/ PRIOR FILING DATE: 2000-07-28
/ NUMBER OF SEQ ID NOS: 125
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 89
/ LENGTH: 62
/ TYPE: prt
/ ORGANISM: Conus ermineus
/ US-09-908-741-89

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Query Match 37.4%; Score 46; DB 10; Length 62;
Best Local Similarity 46.7%; Pred. No. 41;
Matches 7; Conservative 2; Mismatches 6; Indels

Qy 5 CCLIPACRRNHKKFC 19
Dy 47 CCSNPACVNVNPOIC 61

RESULT 35

```

US-10-205-823-349
1 Sequence 349, Application US/10205823
2 Publication No. US20030108963A1
3
4 GENERAL INFORMATION:
5 APPLICANT: Schlegel, Robert
6 APPLICANT: Monahan, John E.
7 APPLICANT: Endege, Wilson O.
8 APPLICANT: Gannavarapu, Manjula
9 APPLICANT: Gorbacheva, Bella
10 APPLICANT: Hoersch, Sebastian
11 APPLICANT: Kamatkar, Shubhangi
12 APPLICANT: Womsey, Angela M.
13 APPLICANT: Glatt, Karen
14 APPLICANT: Zhao, Xumei
15 APPLICANT: Anderson, Dustin
16
17 TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
18 TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
19 TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
20
21 FILE REFERENCE: MRI-044
22
23 CURRENT APPLICATION NUMBER: US/10/205,823
24 CURRENT FILING DATE: 2002-07-25
25
26 PRIOR APPLICATION NUMBER: 60/307,982
27 PRIOR FILING DATE: 2001-07-25
28
29 PRIOR APPLICATION NUMBER: 60/314,356
30 PRIOR FILING DATE: 2001-08-22
31
32 PRIOR APPLICATION NUMBER: 60/325,020
33 PRIOR FILING DATE: 2001-12-12
34
35 PRIOR APPLICATION NUMBER: 60/341,746
36 PRIOR FILING DATE: 2002-03-05
37
38 PRIOR APPLICATION NUMBER: 60/362,158
39 PRIOR FILING DATE: 2002-03-05
40
41 NUMBER OF SEQ ID NOS: 455
42
43 SOFTWARE: FastSeq for Windows Version 4.0

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EQ ID NO 349
LENGTH: 185
TYPE: PRT
ORGANISM: Homo sapiens
10-205-823-349

Very Match 37.4%; Score 46; DB 14; Length 185;
Best Local Similarity 43.8%; Pred. NO. 1e+02;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

4 RCCLIPACRRNHKKFC 19
:||||:|:|:
170 KCCLIGTKKSLAKYC 185

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time : 610 secs

GenCore version 5.1.6
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protein - protein search, using sw model

on: February 18, 2004, 06:03:18 : Search time 42 Seconds
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US-09-806-376-1

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al number of hits satisfying chosen parameters: 389414

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mm DB seq length: 2000000000

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Maximum Match 100%

Listing first 50 summaries

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2: /cgn2_6/prodata/2/aa/5B_COMB.pep.*

3: /cgn2_6/prodata/2/aa/5A_COMB.pep.*

4: /cgn2_6/prodata/2/aa/6B_COMB.pep.*

5: /cgn2_6/prodata/2/aa/PCITS_COMB.pep.*

6: /cgn2_6/prodata/2/aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Alt	Score	Query	Match	Length	DB	ID	Description
1	50	40.7	70	1	US-08-137-800-49		Sequence 49, Appl
2	50	40.7	70	1	US-08-477-383-49		Sequence 49, Appl
3	50	40.7	70	1	US-08-487-174-49		Sequence 49, Appl
4	50	40.7	70	1	US-08-480-750-49		Sequence 49, Appl
5	50	40.7	398	4	US-09-252-991A-26217		Sequence 26217, A
6	49	39.8	101	4	US-09-252-991A-20226		Sequence 20226, A
7	48	39.0	16	3	US-09-219-446B-9		Sequence 9, Appl
8	48	39.0	226	4	US-09-252-991A-23844		Sequence 23844, A
9	48	39.0	234	4	US-09-270-391-16		Sequence 16, Appl
10	47	38.2	16	3	US-09-219-446B-10		Sequence 10, Appl
11	46	37.4	18	1	US-08-137-800-32		Sequence 32, Appl
12	46	37.4	18	1	US-08-477-383-32		Sequence 32, Appl
13	46	37.4	18	1	US-08-487-174-32		Sequence 32, Appl
14	46	37.4	24	1	US-08-480-750-32		Sequence 32, Appl
15	46	37.4	24	1	5464756-3		Patent No. 5464756
16	46	37.4	62	3	US-09-488-799-89		Sequence 89, Appl
17	46	37.4	185	3	US-08-950-720A-13		Sequence 13, Appl
18	46	37.4	317	3	US-08-461-607-2		Sequence 2, Appl
19	46	37.4	317	3	US-09-363-600-2		Sequence 2, Appl
20	45	36.6	58	1	US-08-344-695-10		Sequence 10, Appl
21	45	36.6	77	4	US-09-621-976-4938		Sequence 4938, Ap
22	45	36.6	280	4	US-09-352-991A-30950		Sequence 30950, A
23	45	36.6	589	1	US-07-668-648-2		Sequence 2, Appl
24	45	36.6	589	1	US-08-429-998-2		Sequence 2, Appl
25	45	36.6	589	2	US-08-431-333-2		Sequence 2, Appl
26	45	36.6	589	5	PCT-US91-02321-2		Sequence 2, Appl
27	45	36.6	593	1	US-07-668-648-4		Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-08-137-800-49
; Sequence 49, Application US/08137800
; Patent No. 5514774
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Hillyard, David R.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Santos, Ameurina D
; TITLE OF INVENTION: Conotoxin Peptides
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue N.W., Suite 1000
; CITY: Washington
; STATE: DC
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,800
; FILING DATE: 19-OCT-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24260-104763
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Conus sulcatus
US-08-137-800-49

Sequence 4, Appli
Sequence 4, Appli
Sequence 17, Appl
Sequence 4, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 54, Appl
Sequence 54, Appl
Sequence 54, Appl
Sequence 2, Appli
Sequence 3, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 6430, Ap
Sequence 93, Appl
Sequence 97, Appl
Sequence 99, Appl
Sequence 48, Appl
Sequence 48, Appl
Sequence 48, Appl

Query Match 40.7%; Score 50; DB 1; Length 70;
 Best Local Similarity 46.7%; Pred. No. 7.5;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19
 |||||:
 52 CCSFPACRKYRPMC 66

JLT 2

08-477-383-49
 Sequence 49, Application US/08477383
 Patent No. 5589340

GENERAL INFORMATION:
 APPLICANT: Olivera, Baldomero M.
 APPLICANT: Cruz, Lourdes J.
 APPLICANT: Hillyard, David R.
 APPLICANT: Macintosh, J. Michael
 APPLICANT: Santos, Ameurfino S.
 TITLE OF INVENTION: Conotoxin Peptides
 NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti
 STREET: 1201 New York Avenue, N.W., Suite 1000
 CITY: Washington
 STATE: DC
 COUNTRY: U.S.A.
 ZIP: 20005

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/477,383
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/137,800
 FILING DATE: 19-OCT-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/084,848
 FILING DATE: 29-JUN-1993

ATTORNEY/AGENT INFORMATION:
 NAME: Ihnen, Jeffrey L.
 REGISTRATION NUMBER: 28,957
 REFERENCE/DOCKET NUMBER: 24260-107673
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-962-4810
 TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 49:

SEQUENCE CHARACTERISTICS:
 LENGTH: 70 amino acids
 TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Conus sulcatus

08-477-383-49

Query Match 40.7%; Score 50; DB 1; Length 70;
 Best Local Similarity 46.7%; Pred. No. 7.5;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19
 |||||:
 52 CCSFPACRKYRPMC 66

JULT 3

US-08-487-174-49
 Sequence 49, Application US/08487174
 Patent No. 5595972

GENERAL INFORMATION:
 APPLICANT: Olivera, Baldomero M.
 APPLICANT: Cruz, Lourdes J.
 APPLICANT: Hillyard, David R.
 APPLICANT: Macintosh, J. Michael
 APPLICANT: Santos, Ameurfino S.
 TITLE OF INVENTION: Conotoxin Peptides
 NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti
 STREET: 1201 New York Avenue, N.W., Suite 1000
 CITY: Washington
 STATE: DC
 COUNTRY: U.S.A.
 ZIP: 20005

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/487,174
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 514

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/137,800
 FILING DATE: 19-OCT-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/084,848
 FILING DATE: 29-JUN-1993

ATTORNEY/AGENT INFORMATION:
 NAME: Ihnen, Jeffrey L.
 REGISTRATION NUMBER: 28,957
 REFERENCE/DOCKET NUMBER: 24260-107673
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-962-4810
 TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 49:

SEQUENCE CHARACTERISTICS:
 LENGTH: 70 amino acids
 TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Conus sulcatus

US-08-487-174-49

Query Match 40.7%; Score 50; DB 1; Length 70;
 Best Local Similarity 46.7%; Pred. No. 7.5;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Oy 5 CCLIPACRRNHKKFC 19
 |||||:
 Db 52 CCSFPACRKYRPMC 66

RESULT 4

US-08-480-750-49
 Sequence 49, Application US/08480750
 Patent No. 5633347

GENERAL INFORMATION:
 APPLICANT: Olivera, Baldomero M.
 APPLICANT: Cruz, Lourdes J.
 APPLICANT: Hillyard, David R.
 APPLICANT: Macintosh, J. Michael
 APPLICANT: Santos, Ameurfino S.
 TITLE OF INVENTION: Conotoxin Peptides
 NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:
ADDRESSES: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/480,750
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993

ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 24260-107673
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810

TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 49:

SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear

MOLECULE TYPE: peptide
HYPOTHETICAL: NO

ORIGINAL SOURCE:
ORGANISM: Conus sulcatus

38-480-750-49

Very Match 40.7%; Score 50; DB 1; Length 70;
Best Local Similarity 46.7%; Pred. No. 7.5;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19
||| ||||| :
52 CCSFPACKRYPEMC 66

ULT 5
09-252-991A-26217
Sequence 26217, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A

PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190

NUMBER OF SEQ ID NOS: 33142
EQ ID NO 26217

LENGTH: 398
TYPE: PRT

ORGANISM: Pseudomonas aeruginosa
09-252-991A-26217

Very Match 40.7%; Score 50; DB 4; Length 398;

Best Local Similarity 52.9%; Pred. No. 32;
Matches 9; Conservative 1; Mismatches 3; Indels 4; Gaps 1;

QY 3 WRCCLPACRRNHKKFC 19
||| ||||| :
Db 59 WRCC---CRSPKGC 71

RESULT 6
US-09-252-991A-20226
Sequence 20226, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A

PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190

NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20226

LENGTH: 101
TYPE: PRT

ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20226

Query Match 39.8%; Score 49; DB 4; Length 101;
Best Local Similarity 72.7%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 WRCCLPACRR 13
||| ||||| :
Db 88 WRCGTTPACRR 98

RESULT 7
US-09-219-446B-9
Sequence 9, Application US/09219446B
Patent No. 6265541

GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.

APPLICANT: McIntosh, J. Michael

APPLICANT: Yoshikami, Doju

APPLICANT: Cartier, G. Edward

APPLICANT: Luo, Siqin

APPLICANT: University of Utah Research Foundation

TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides

FILE REFERENCE: Uses of Alpha-Conotoxins

CURRENT APPLICATION NUMBER: US/09/219,446B

CURRENT FILING DATE: 1998-12-23

PRIOR APPLICATION NUMBER: US 60/080,598

PRIOR FILING DATE: 1998-04-03

PRIOR APPLICATION NUMBER: US 60/070,153

PRIOR FILING DATE: 1997-12-31

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patent in Ver. 2.0

SEQ ID NO 9

LENGTH: 16

TYPE: PRT

ORGANISM: Conus purpurascens

US-09-219-446B-9

Query Match 39.0%; Score 48; DB 3; Length 16;
Best Local Similarity 40.0%; Pred. No. 3.9;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19
||| ||||| :
Db 2 CCSLPCCANNPDYC 16

ULT 8
09-252-991A-23844
sequence 23844, Application US/09252991A
atent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
EQ ID NO 23844
LENGTH: 226
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
09-252-991A-23844
Query Match 39.0%; Score 48; DB 4; Length 226;
est Local Similarity 77.8%; Pred. No. 36;
atches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
2 NWRCLLIPA 10
100 NWRCCASPA 108
ULT 9
09-270-391-16
sequence 16, Application US/09270391A
atent No. 6410233
GENERAL INFORMATION:
APPLICANT: de Belle, Ian
APPLICANT: Adamson, Eileen
APPLICANT: Mergola, Dan
TITLE OF INVENTION: Isolation and Identification of Control Sequences and
FILE REFERENCE: PS-00101.P.1
CURRENT APPLICATION NUMBER: US/09/270,391A
CURRENT FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 16
LENGTH: 234
TYPE: PRT
ORGANISM: Homo sapiens
09-270-391-16
Query Match 39.0%; Score 48; DB 4; Length 234;
est Local Similarity 57.1%; Pred. No. 37;
atches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
2 NWRCLLPACRNH 15
6 DYRCCLPPATHPH 19
ULT 10
09-219-446B-10
Sequence 10, Application US/09219446B
Patent No. 6265541
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Yoshikami, Doju
APPLICANT: Cartier, G. Edward
APPLICANT: Luo, Siqin

APPLICANT: University of Utah Research Foundation
TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
FILE REFERENCE: Uses of Alpha-Conotoxins
CURRENT APPLICATION NUMBER: US/09/219,446B
CURRENT FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 60/080,588
PRIOR FILING DATE: 1998-04-03
PRIOR APPLICATION NUMBER: US 60/070,153
PRIOR FILING DATE: 1997-12-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 10
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: A10L derivative
OTHER INFORMATION: of C. purpurascens PnIA
US-09-219-446B-10
Query Match 38.2%; Score 47; DB 3; Length 16;
Best Local Similarity 40.0%; Pred. No. 5.2;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 5 CCLIPACRNHHKFC 19
DB 2 CCSLPPCALNPDYC 16
RESULT 11
US-08-137-800-32
Sequence 32, Application US/08137800
Patent No. 5514774
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: McIntosh, J. Michael
APPLICANT: Santos, Aneurquina D.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1000
CITY: Washington
STATE: DC
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,800
FILING DATE: 19-OCT-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-104763
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Conus ermineus


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FEATURE:
NAME/KEY: Modified-site
LOCATION: 3..4
OTHER INFORMATION: /note= "Xaa is Pro or Hydroxy-Pro"
18-137-800-32
Query Match 37.4%; Score 46; DB 1; Length 18;
Best Local Similarity 46.7%; Pred. No. 7.7;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19
||| ||| ||| :|
4 CCSNPACVNNPQIC 18

PAT 12
18-477-383-32
Sequence 32, Application US/08477383
Patent No. 5589340
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hilliard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurfino S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,383
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Conus ermineus
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /note= "Xaa is Pro or Hydroxy-Pro."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 18
OTHER INFORMATION: /note= "The C-terminus is
preferably amidated."

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;
; OTHER INFORMATION: /note= "The C-terminus is
; OTHER INFORMATION: preferably amidated."
US-08-477-383-32
Query Match 37.4%; Score 46; DB 1; Length 18;
Best Local Similarity 46.7%; Pred. No. 7.7;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19
||| ||| ||| :|
Db 4 CCSNPACVNNPQIC 18

RESULT 13
US-08-487-174-32
Sequence 32, Application US/08487174
Patent No. 5595972
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hilliard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurfino S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,174
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Conus ermineus
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /note= "Xaa is Pro or Hydroxy-Pro."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 18
OTHER INFORMATION: /note= "The C-terminus is
preferably amidated."

```

5 CCLIPACRRNHKKFC 19
4 CCSNPACNVNPNPOIC 18

ULT 17
08-950-720A-13
Sequence 13, Application US/08950720A
Patent No. 6046028
GENERAL INFORMATION:
APPLICANT: Conklin, Darrell C.
APPLICANT: Lofton-Day, Catherine E.
APPLICANT: Lok, Si
TITLE OF INVENTION: Jaspers, Stephen R.
TITLE OF INVENTION: INSULIN HOMOLOG
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/950,720A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-09
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6046028e
08-950-720A-13
Query Match 37.4%; Score 46; DB 3; Length 185;
Best Local Similarity 43.8%; Pred. No. 55;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
4 RCCLIPACRNHHKFC 19
:||||:|:|:
170 KCCLIGCTKSLAKYC 185

ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,607
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/379,105
FILING DATE:
APPLICATION NUMBER: US 07/874,974
FILING DATE: 27-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-461-607-2
Query Match 37.4%; Score 46; DB 3; Length 317;
Best Local Similarity 66.7%; Pred. No. 87;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 3 WECCLIPACRN 14
DB 36 WRCCLIPRRRD 47
RESULT 19
US-09-363-600-2
Sequence 2, Application US/09363600
Patent No. 6232524
GENERAL INFORMATION:
APPLICANT: Tischfield, Jay A.
APPLICANT: Stambrook, Peter J.
TITLE OF INVENTION: Live Animal Mutagenesis Systems for
TITLE OF INVENTION: Testing Mutagenic Agents in Vivo
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
ADDRESSEE: Russell, P.A.
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
STATE: FL
COUNTRY: USA
ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,600
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,607
FILING DATE:
APPLICATION NUMBER: US 07/874,974
FILING DATE: 27-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.

REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 305-527-2498

TELEFAX: 305-764-4996

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 317 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

39-363-600-2

Query Match 37.4%; Score 46; DB 3; Length 317;
Best Local Similarity 66.7%; Pred. No. 87;

atches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

3 WRCLIPACRN 14

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36 WRCLIPRRRD 47

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ULT 20

08-344-695-10

sequence 10 Application US/08344695

agent No. 5614398

GENERAL INFORMATION:

APPLICANT: O'BROCHTA, DAVID

APPLICANT: WARREN, WILLIAM

APPLICANT: ATKINSON, PETER

TITLE OF INVENTION: A GENE TRANSFER SYSTEM FOR INSECTS

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,

ADDRESSEE: P.C.

STREET: 1755 S. Jefferson Davis Highway, Suite 400

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/344,695

FILING DATE: 18-NOV-1994

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Kelber, Steven B.

REGISTRATION NUMBER: 30,073

REFERENCE/DOCKET NUMBER: 2747-058-27

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 58 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: peptide

08-344-695-10

Query Match 36.6%; Score 45; DB 1; Length 58;

Best Local Similarity 44.4%; Pred. No. 28;

atches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

2 NWRCLIPACRNHKFC 19

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2 NWAQCLLCFTRYSHKTC 19

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RESULT 21

US-09-621-976-4938

; Sequence 4938, Application US/09621976

; Patent No. 6639063

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Jobert, S.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

; FILE REFERENCE: GENSET.054PR2

; CURRENT APPLICATION NUMBER: US/09/621,976

; CURRENT FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 19335

; SOFTWARE: Patent.pm

; SEQ ID NO 4938

; LENGTH: 77

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: UNSURE

; LOCATION: 20

; OTHER INFORMATION: Xaa = Met,Arg

US-09-621-976-4938

Query Match 36.6%; Score 45; DB 4; Length 77;

Best Local Similarity 50.0%; Pred. No. 35;

Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 WRCLIPACRNHK 16

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Db 8 WRCCCNFLCKRXXK 21

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RESULT 22

US-09-252-991A-30950

; Sequence 30950, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 30950

; LENGTH: 280

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-30950

Query Match 36.6%; Score 45; DB 4; Length 280;

Best Local Similarity 53.8%; Pred. No. 1.1e+02;

Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 RCCCLIPACRNHK 16

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Db 61 RCCAGPACARSRR 73

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RESULT 23

US-07-668-648-2

; Sequence 2, Application US/07668648

; Patent No. 5416192

; GENERAL INFORMATION:

; APPLICANT: Shoyab, Mohammed

; APPLICANT: Flowman, Gregory D.

1030
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,998
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:

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383 DWGCCPIPEAVCCLDHQCC 402

ULT 26

US91-02321-2
Sequence 2, Application PC/TUS9102321
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
TITLE OF INVENTION: EPIITHELINS: NOVEL CYSTEINE-RICH GROWTH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212) 869-9741
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:

ADDRESSEE: Bristol-Myers Squibb Company
STREET: 3005 First Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US91/02321
FILING DATE: 19910403
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Poor, Brian W.

REGISTRATION NUMBER: 32,928

REFERENCE/DOCKET NUMBER: ON0071A-PC

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)728-4800

TELEFAX: (206)448-4775

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 589 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

US91-02321-2

Query Match 36.6%; Score 45; DB 5; Length 589;
Best Local Similarity 40.0%; Pred. No. 2e+02;
Matches 8; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

2 NWRCCLIP--ACRRNHKFC 19

|||||

383 DWGCCPIPEAVCCLDHQCC 402

ULT 27

US91-02321-2
Sequence 4, Application US/07668648
Patent No. 5416192

GENERAL INFORMATION:

APPLICANT: Shoyab, Mohammed

REGISTRATION NUMBER: 32,928

TITLE OF INVENTION: EPIITHELINS: NOVEL CYSTEINE-RICH GROWTH

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)790-9090

TELEFAX: (212) 869-9741

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/668,648

FILING DATE: 19910819

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 5624-161-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)790-9090

TELEFAX: (212) 869-9741

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 593 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-668-648-4

Query Match 36.6%; Score 45; DB 1; Length 593;
Best Local Similarity 42.1%; Pred. No. 2e+02;
Matches 8; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

QY 3 WRCCCLIP--ACRRNHKFC 19

|||||

Db 386 WGCCPIPEAVCCLDHQCC 404

RESULT 28

US-08-429-998-4

Sequence 4, Application US/08429998

Patent No. 5885961

GENERAL INFORMATION:

APPLICANT: Shoyab, Mohammed

REGISTRATION NUMBER: 32,928

TITLE OF INVENTION: EPIITHELINS: NOVEL CYSTEINE-RICH GROWTH

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)790-9090

TELEFAX: (212) 869-9741

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/429,998

FILING DATE: 27-APR-1995

CLASSIFICATION: 514

Prior Application Number: US 07/668,648

ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 5624-161-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)790-9090

TELEFAX: (212) 869-9741

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 593 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-429-998-4

ed Feb 18 06:30:56 2004

Very Match	36.6%	Score 45;	DB 2;	Length 593;
1st Local Similarity	42.1%;	Pred. No. 2e+02;		
atches	8;	Conservative	2;	Mismatches
			7;	Indels
			2;	Gaps
				1;

3 WRCLIP--ACRRNHKKFC 19
| | | | | : : |
386 WGCCPIPEAVCCSDHOHCC 404

IUT 29
 18-431-333-4
 Sequence 4, Application US/08431333
 Patent No. 5965723
 GENERAL INFORMATION:
 APPLICANT: Shoyab, Mohammed
 APPLICANT: Gregory D.
 TITLE OF INVENTION: BITHIELINS: NOVEL CYSTEINE-RICH GROWTH
 TITLE OF INVENTION: MODULATING PROTEINS
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA

very Match	36.6%;	Score 45;	DB 2;	Length 593;
est Local Similarity	42.1%;	Pred. No. 2e+02;		
atches	8: Conservative	2: Mismatches	7: Indels	2: Gaps

```

3 WRCCCLIP--ACRRNHKKFC 19
      ||||| : : |
386 WCCCPIDFAYCCSDHWHCC 404

```

JLT 30
 08-991-862-17
 sequence 17, Application US/08991862
 atent No. 6309826
 GENERAL INFORMATION:
 APPLICANT: Serriezo, Ginette
 TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
 FILE REFERENCE: Z9996.488/P001-A
 CURRENT APPLICATION NUMBER: US/08/991.862
 CURRENT FILING DATE: 1998-08-17
 EARLIER APPLICATION NUMBER: 08/863.862

```

; EARLIER FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 17
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Human GP88 CDNA
US-08-991-852-17

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Query Match      36.6%; Score 45; DB 4; Length 593;
Best Local Similarity 42.1%; Pred. No. 2e+02;
Matches      8; Conservative      2; Mismatches      7; Indels      2; Gaps      1;
```

QY 3 WRCLIP--ACRRNHKKFC 19
DB 386 WGCCPIPEAVCCSDHOHCC 404

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RESULT 31
US-09-813-156-17
; Sequence 17, Application US/09813156
; Patent No. 6670183
; GENERAL INFORMATION:
; APPLICANT: Serrero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: Z3996.488/P001-A
; CURRENT APPLICATION NUMBER: US/09/813,156
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 08/991,862
; PRIOR FILING DATE: 1997-12-16
; PRIOR APPLICATION NUMBER: 08/863,862
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Human GP88 cdNA
US-09-813-156-17

```

Query Match 36.6%; Score 45; DB 4; Length 593;
Best Local Similarity 42.1%; Pred. No. 2e+02;
Matches 8; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

QY 3 WRCLIP--ACRRNHKKFC 19
DB 386 WGCGPIPEAVCCSDHOHCC 404

RESULT 32
PCT-US91-02321-4
Sequence 4, Application PC/TUS9102321
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPIITELING: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company
STREET: 3005 First Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patattin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02321
FILING DATE: 19910403

```
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Poor, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: 080071A-PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)728-4800
TELEFAX: (206)448-4775
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acids
TYPE: AMINO ACID
MOLECULE TYPE: protein
TOPOLOGY: linear
-MUS91-02321-4

Query Match 36.6%; Score 45; DB 5; Length 593;
Best Local Similarity 42.1%; Pred. No. 2e+02;
Matches 8; Conservative 2; Mismatches 7; Indels 7; Gaps 1;

3 WRCCLP--ACRRNHKKFC 19
386 WGCCPIEAVCCSDHQC 404

ULT 33
09-029-047C-2
sequence 2, Application US/09029047C
Patent No. 683236
GENERAL INFORMATION:
APPLICANT: Carr, Antony M.
TITLE OF INVENTION: Cell-Cycle Checkpoint Genes
FILE REFERENCE: 27866/34132
CURRENT APPLICATION NUMBER: US/09/029,047C
CURRENT FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: PCT/GB96/02197
PRIOR FILING DATE: 1996-09-06
PRIOR APPLICATION NUMBER: GB 9518220.0
PRIOR FILING DATE: 1995-09-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patent in Ver. 3.1
EQ ID NO 2
LENGTH: 2644
TYPE: PRT
ORGANISM: Homo sapiens
09-029-047C-2

Query Match 36.6%; Score 45; DB 4; Length 2644;
Best Local Similarity 37.5%; Pred. No. 7e+02;
Matches 9; Conservative 1; Mismatches 8; Indels 6; Gaps 1;

2 NW-----RCCLIPACRRNHKKFC 19
101 NWIITRLIRIAATPSCHLLHKIC 124

ULT 34
08-801-344-4
Sequence 4, Application US/08801344
Patent No. 6087140
GENERAL INFORMATION:
APPLICANT: Cameron, Douglas C.
APPLICANT: Shaw, Anita J.
APPLICANT: Altaras, Nedim E.
TITLE OF INVENTION: MICROBIAL PRODUCTION OF 1,2-PROPANEDIOL
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: Dewitt Ross & Stevens S.C.
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
STATE: WI
COUNTRY: U.S.A.

ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,599
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REFERENCE/DOCKET NUMBER: 09820.037
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-831-2100
TELEFAX: 608-831-2106
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Rat lens aldose reductase
US-08-801-344-4

Query Match 36.2%; Score 44.5; DB 3; Length 316;
Best Local Similarity 41.2%; Pred. No. 1.4e+02;
Matches 7; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 2 NWRCCLPACRRNHKKF 18
DB 295 NNRVCALMSCAK-HKDY 310

RESULT 35
US-09-498-599-4
Sequence 4, Application US/09498599
Patent No. 6303352
GENERAL INFORMATION:
APPLICANT: Cameron, Douglas C.
APPLICANT: Shaw, Anita J.
APPLICANT: Altaras, Nedim E.
TITLE OF INVENTION: MICROBIAL PRODUCTION OF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: Dewitt Ross & Stevens S.C.
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
STATE: WI
COUNTRY: U.S.A.
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,599
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REFERENCE/DOCKET NUMBER: 09820.037
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-831-2100
TELEFAX: 608-831-2106
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
```


LENGTH: 316 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Rat lens aldose reductase
99-498-599-4
very Match 36.2%; Score 44.5; DB 4; Length 316;
sst Local Similarity 41.2%; Pred. No. 1.4e+02;
atches 7; Conservative 4; Mismatches 5; Indels 1; Gaps 1;
2 NWRCCCLIPACRRNHKXF 18
||| : : : :
295 NWRVCAIMSCAK-HKDY 310
rch completed: February 18, 2004, 06:08:05
time : 43 secs

GenCore version 5.1.6
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protein - protein search, using sw model

on: February 18, 2004, 06:16:09 ; Search time 21 Seconds
(without alignments)
87.030 Million cell updates/sec

le: US-09-806-376-1

fect score: 123

uence: 1 FNRCCCLIPACRRNHKKFC 19

bring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 283366 seqs, 96191526 residues

al number of hits satisfying chosen parameters: 3435

imum DB seq length: 0

imum DB seq length: 19

st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

atabase : PIR 78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

alt	No.	Score	Query Match	Length	DB ID	Description
1	48	39.0	16	2	A54877	alpha-conotoxin Pn
2	44	35.8	16	2	A59046	alpha-conotoxin MI
3	44	35.8	16	2	A59042	alpha-conotoxin Ep
4	42	34.1	16	2	B54877	alpha-conotoxin Pn
5	40	32.5	18	1	A58589	alpha-conotoxin EI
6	38	30.9	16	2	A59045	alpha-conotoxin Au
7	38	30.9	19	2	A44379	alpha-conotoxin SI
8	37.5	30.5	14	1	NTKNLM	alpha-conotoxin MI
9	37	30.1	16	2	C59045	alpha-conotoxin Au
10	31	25.2	13	1	NTKNAS	alpha-conotoxin SI
11	31	25.2	15	1	NTKNAG	alpha-conotoxin GI
12	30	24.4	15	2	B59045	alpha-conotoxin Au
13	29.5	24.0	14	2	A58963	alpha-conotoxin Cn
14	28	22.8	12	1	A53709	alpha-conotoxin Im
15	27.5	22.4	17	2	A54534	heat-stable entero
16	27	22.0	16	2	PH1781	T cell receptor al
17	27	22.0	18	1	QHEC2	heat-stable entero
18	26	21.1	9	2	A29477	diuretic neuropt
19	26	21.1	12	2	A33900	hydrin 1 - African
20	26	21.1	13	1	NTKN2G	alpha-conotoxin GI
21	26	21.1	19	2	C21182	4K prothoracitro
22	25.5	20.7	18	2	A60103	heat-stable entero
23	25	20.3	13	2	A28953	alpha-conotoxin SI
24	24	19.5	8	2	A54823	olfactory receptor
25	24	19.5	8	2	B54823	olfactory receptor
26	24	19.5	11	2	S61797	T-cell-specific tr
27	24	19.5	19	2	A58700	actagardine [valid
28	23	18.7	19	2	B28495	conopressin S - co
29	23	18.7	11	2	T06383	hypothetical prote

hypothetical prote
hypothetical prote
hypothetical prote
manganese peroxida
gene Ctr protein
deoxynucleotidyltr
hypothetical prote
epsilon receptor m
4K prothoracitro
manganese peroxida
arginine vasotocin
vasotocin - common
hydrin 2 - bullfro
urotensin II - lon
urotensin II - tel
urotensin II-A pep
urotensin II-B pep
urotensin II - lau
lutropin beta chai
Ig H chain V-D-J r
hypothetical prote

ALIGNMENTS

RESULT 1

A54877
alpha-conotoxin PnIA [validated] - cone shell (Conus pennaceus)

NAlternate names: alpha-Crx-PnIA

C:Species: Conus pennaceus

C>Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 15-Sep-2000

C:Accession: A54877

R:Painzilber, M.; Hasson, A.; Oren, R.; Burlingame, A.L.; Gordon, D.; Spira, M.E.; Zlot

Biochemistry 33, 9523-9529, 1994

A>Title: New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine rec

A:Reference number: A54877; MUID:94347719; PMID:8068627

A:Accession: A54877

A:Molecule type: protein

A:Residues: 1-16 <FAI>

R:Hu, S.H.; Gehrmann, J.; Guddat, L.W.; Alewood, P.F.; Craik, D.J.; Martin, J.L.

submitted to the Brookhaven Protein Data Bank, January 1996

A:Reference number: A6355; PDB:13EN

A:Content: amotiation; X-ray crystallography, 1.1 angstroms; residues 1-16

C:Superfamily: alpha-conotoxin

C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neurc

F:2-8,3-16/Disulfide bonds: #status experimental

F:16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 39.0%; Score 48; DB 2; Length 16;

Best Local Similarity 40.0%; Fred. NO. 1.6;

Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19

Db 2 CCSLPCCANNPDYC 16

RESULT 2

A59046

alpha-conotoxin MII - cone shell (Conus magus)

C:Species: Conus magus (magus cone)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C:Accession: A59046

R:Cartier, G.E.; Foshikami, D.; Gray, W.R.; Luo, S.; Olivera, B.M.; McIntosh, J.M.

J. Biol. Chem. 271, 7522-7528, 1996

A>Title: A new alpha-conotoxin which targets alpha3beta2 nicotinic acetylcholine recept

A:Reference number: A59046; MUID:96205934; PMID:8631783

A:Accession: A59046

A>Status: Preliminary

A:Molecule type: protein

A:Residues: 1-16 <CAR>

Superfamily: alpha-conotoxin
 Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro
 1-16/Product: alpha-conotoxin MII #status experimental <MAT>
 2-8,3-16/Disulfide bonds: #status experimental
 16/Modified site: amidated carboxyl end (Cys) #status experimental
 Query Match 35.8%; Score 44; DB 2; Length 16;
 Best Local Similarity 40.0%; Pred. No. 6.1;
 Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 5 CCLIPACRRNHKKFC 19
 2 CCNPFVCHLEHNL 16

SULT 3
 9042
 Superfamily: alpha-conotoxin
 Keywords: alpha-conotoxin Epi - cone shell (Conus episcopatus)
 Species: Conus episcopatus (bishop's cone)
 Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 13-Aug-1999
 Accession: A59042
 Loughnan, M.; Bond, T.; Atkins, A.; Cuevas, J.; Adams, D.J.; Broxton, N.M.; Livett, B.
 Biol. Chem. 273, 15667-15674, 1998
 Title: Alpha-conotoxin Epi, a novel sulfated peptide from Conus episcopatus that sele
 Reference number: A59042; MUID:98288307; PMID:9624161
 Accession: A59042
 Status: preliminary
 Molecule type: protein
 Residues: 1-16 <LOU>
 Superfamily: alpha-conotoxin
 Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro
 1-16/Product: alpha-conotoxin Epi #status experimental <MAT>
 2-8,3-16/Disulfide bonds: #status experimental
 15/Binding site: sulfate (Tyr) (covalent) #status experimental
 16/Modified site: amidated carboxyl end (Cys) #status experimental
 Query Match 35.8%; Score 44; DB 2; Length 16;
 Best Local Similarity 40.0%; Pred. No. 6.1;
 Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
 5 CCLIPACRRNHKKFC 19
 2 CCSDPRCNWNPDYC 16

RESULT 4
 14877
 Superfamily: alpha-conotoxin
 Keywords: alpha-conotoxin PnIB - cone shell (Conus pennaceus)
 Species: Conus pennaceus
 Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-May-1997
 Accession: B54877
 Faiznilber, M.; Haason, A.; Oren, R.; Burlingame, A.L.; Gordon, D.; Spira, M.E.; Zlotk
 lochemistry 33, 9523-9529, 1994
 Title: New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine rece
 Reference number: A54877; MUID:94347719; PMID:8068627
 Accession: B54877
 Status: preliminary
 Molecule type: protein
 Residues: 1-16 <FAI>
 Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynap
 Superfamily: alpha-conotoxin
 Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro
 1-16/Product: alpha-conotoxin PnIB #status experimental
 2-8,3-16/Disulfide bonds: #status experimental
 16/Modified site: amidated carboxyl end (Cys) #status experimental
 Query Match 34.1%; Score 42; DB 2; Length 16;
 Best Local Similarity 33.3%; Pred. No. 12;
 Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 5 CCLIPACRRNHKKFC 19
 2 CCNPFVCHLEHNL 16

RESULT 5
 A58589
 Superfamily: alpha-conotoxin EI - cone shell (Conus ermineus)
 Species: Conus ermineus (ermine cone)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C/Accession: A58589
 R/Martinez, J.S.; Olivera, B.M.; Gray, W.R.; Craig, A.G.; Groebe, D.R.; Abramson, S.N.,
 Biochemistry 34, 14519-14526, 1995
 A/Title: alpha-Conotoxin EI, a new nicotinic acetylcholine receptor antagonist with nov
 A/Reference number: A58589; MUID:96062516; PMID:7578057
 A/Accession: A58589
 A/Molecule type: protein
 A/Residues: 1-18 <MAR>
 A/Note: sequence confirmed by chemical synthesis
 C/Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynap
 C/Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; hydroxyproline; pc
 F/3/Modified site: 4-hydroxyproline (Pro) #status experimental
 F/4-10,5-18/Disulfide bonds: #status experimental
 F/18/Modified site: amidated carboxyl end (Cys) #status experimental
 Query Match 32.5%; Score 40; DB 1; Length 18;
 Best Local Similarity 33.3%; Pred. No. 25;
 Matches 5; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 QY 5 CCLIPACRRNHKKFC 19
 DB 4 CCYHPTCNWNPQIC 18

RESULT 6
 A59045
 Superfamily: alpha-conotoxin AuiA - cone shell (Conus aulicus)
 Species: Conus aulicus (court cone)
 C/Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999
 C/Accession: A59045
 R/Luo, S.; Kulak, J.M.; Cartier, G.E.; Jacobsen, R.B.; Yoshikami, D.; Olivera, B.M.; Mc
 J. Neurosci. 18, 8571-8579, 1998
 A/Title: Alpha-conotoxin AuiB selectively blocks alpha3beta4 nicotinic acetylcholine re
 A/Reference number: A59045; MUID:99003392; PMID:9786965
 A/Accession: A59045
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-16 <LOO>
 C/Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro
 F/1-16/Product: alpha-conotoxin AuiA #status experimental <MAT>
 F/2-8,3-16/Disulfide bonds: #status experimental
 F/16/Modified site: amidated carboxyl end (Cys) #status experimental
 Query Match 30.9%; Score 38; DB 2; Length 16;
 Best Local Similarity 33.3%; Pred. No. 44;
 Matches 5; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 QY 5 CCLIPACRRNHKKFC 19
 DB 2 CCNPFVCHLEHNL 16

RESULT 7
 A44379
 Superfamily: alpha-conotoxin SII - cone shell (Conus striatus)
 Species: Conus striatus (striated cone)
 C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
 C/Accession: A44379
 R/Ramilo, C.A.; Zafaralla, G.C.; Nadaedi, L.; Hammerland, L.G.; Yoshikami, D.; Gray, W
 Biochemistry 31, 9919-9926, 1992
 A/Title: Novel alpha- and omega-conotoxins from Conus striatus venom.
 A/Reference number: A44379; MUID:93003172; PMID:1390774
 A/Accession: A44379
 A/Molecule type: protein
 A/Residues: 1-19 <RAM>
 A/Cross-references: CAS:143294-31-9; PIDN:AAB23762.1; PID:g257934

Experimental source: venom
 Note: sequence extracted from NCBI backbone (NCBIP:116000); structure confirmed by chemo
 Comment: This peptide is an acetylcholine receptor blocker.
 Superfamily: alpha-conotoxin
 Keywords: acetylcholine receptor inhibitor; postsynaptic neurotoxin; venom
 -18,3-4-14/Disulfide bonds: #status predicted
 9/Modified site: amidated carboxyl end (Ser) #status absent

Query Match 30.9%; Score 38; DB 2; Length 19;
 Best Local Similarity 54.5%; Pred. No. 50;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

5 CCLIPACRRNH 15
 |||||
 2 CCNCPACGPNY 12

ULT 8
 NIM

Alpha-conotoxin MI - cone shell (Conus magus)
 Species: Conus magus (magus cone)
 Date: 18-Apr-1984 #sequence_revision 18-Apr-1984 #text_change 16-Jul-1999
 Accession: A01784
 McIntosh, M.; Cruz, L.J.; Hunkapiller, M.W.; Gray, W.R.; Olivera, B.M.
 J. Biochem. Biophys. 218, 329-334, 1992
 Title: Isolation and structure of a peptide toxin from the marine snail Conus magus.
 Reference number: A90071; MUID:83073458; PMID:7149738
 Accession: A01784
 Molecule type: protein
 Residues: 1-14 <NCI>
 Gray, W.R.; Rivier, J.E.; Galyean, R.; Cruz, L.J.; Olivera, B.M.
 Biol. Chem. 258, 12247-12251, 1983
 Title: Conotoxin MI Disulfide bonding and conformational states.
 Reference number: A92396; MUID:84032400; PMID:6630187
 Contents: annotation; disulfide bonds
 Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynaptic
 Superfamily: alpha-conotoxin
 Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuroto
 -8-4-14/Disulfide bonds: #status experimental
 4/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 30.5%; Score 37.5; DB 1; Length 14;
 Best Local Similarity 58.3%; Pred. No. 47;
 Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

4 RCCLIPACRRNH 15
 |||||
 2 RCC-HPACGKNY 12

ULT 9
 3045

Alpha-conotoxin AuIC - cone shell (Conus aulicus)
 Species: Conus aulicus (court cone)
 Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999
 Accession: C59045
 Juo, S.; Kulak, J.M.; Cartier, G.E.; Jacobsen, R.B.; Yoshikami, D.; Olivera, B.M.; McI
 Neurosci. 18, 8571-8579, 1998
 Title: Alpha-conotoxin AuIB selectively blocks alpha3beta4 nicotinic acetylcholine rec
 Reference number: A59045; MUID:99003392; PMID:9788965
 Accession: C59045
 Status: preliminary
 Molecule type: protein
 Residues: 1-16 <LUO>
 Superfamily: alpha-conotoxin
 Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro
 1-16/Product: alpha-conotoxin AuIC #status experimental <MAT>
 2-8-3-16/Disulfide bonds: #status experimental
 16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 30.1%; Score 37; DB 2; Length 16;
 Best Local Similarity 33.3%; Pred. No. 61;
 Matches 5; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 5 CCLIPACRRNHKKFC 19
 |||||
 Db 2 CCSVPPCFATNSGYC 16

RESULT 10

NTKNAS

Alpha-conotoxin SIA - cone shell (Conus striatus)

Species: Conus striatus (striated cone)

C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 23-May-1997

C/Accession: A40312

R/Myers, R.A.; Zafaralla, G.C.; Gray, W.R.; Abbott, J.; Cruz, L.J.; Olivera, B.M.

Biochemistry 30, 9370-9377, 1991

A>Title: alpha-Conotoxins, small peptide probes of nicotinic acetylcholine receptors.

A/Reference number: A40312; MUID:91369955; PMID:1892838

A/Accession: A40312

A/Molecule type: protein

A/Residues: 1-13 <MYE>

C/Comment: This paralytic toxin from a fish-hunting cone snail inhibits the acetylcholi

C/Superfamily: alpha-conotoxin

C/Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro

F:2-7,3-13/Disulfide bonds: #status experimental

F:13/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 25.2%; Score 31; DB 1; Length 13;

Best Local Similarity 55.6%; Pred. No. 3.8e+02;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 6 CLIPACRRN 14

|||
 Db 2 CCHPACGKN 10

RESULT 11

NTKNAG

Alpha-conotoxin GIA [validated] - cone shell (Conus geographus)

N/Alternate names: alpha-Crx-GIA

N/Contents: alpha-conotoxin GI

C/Species: Conus geographus (geography cone)

C/Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 15-Sep-2000

C/Accession: A01782

R/Gray, W.R.; Luque, A.; Olivera, B.M.; Barrett, J.; Cruz, L.J.

J. Biol. Chem. 256, 4734-4740, 1981

A>Title: Peptide toxins from Conus geographus venom.

A/Reference number: A92320; MUID:81191854; PMID:7014556

A/Accession: A01782

A/Molecule type: protein

A/Residues: 1-15 <GRA>

R/Gray, W.R.; Rivier, J.E.; Galyean, R.; Cruz, L.J.; Olivera, B.M.

J. Biol. Chem. 258, 12247-12251, 1983

A>Title: Conotoxin MI Disulfide bonding and conformational states.

A/Reference number: A92396; MUID:84032400; PMID:6630187

A/Contents: annotation; disulfide bonds

R/Guddat, L.W.; Shan, L.; Martin, J.L.; Edmundson, A.B.; Gray, W.R.

submitted to the Brookhaven Protein Data Bank, May 1996

A/Reference number: A66253; PDB:1NOT

A/Contents: annotation; X-ray crystallography, 1.2 angstroms, residues 1-13

R/Guddat, L.W.; Martin, J.A.; Shan, L.; Edmundson, A.B.; Gray, W.R.

Biochemistry 35, 11329-11335, 1996

A>Title: Three-dimensional structure of the alpha-conotoxin GI at 1.2 angstroms resolut

A/Reference number: A58592; MUID:96378624; PMID:8784187

A/Contents: annotation; X-ray crystallography, 1.2 angstroms

R/Pardi, A.; Galdes, A.; Florance, J.; Maniccone, D.

Biochemistry 28, 5494-5501, 1989

A>Title: Solution structures of alpha-conotoxin GI determined by two-dimensional NMR sp

A/Reference number: A30629; MUID:89375269; PMID:2775719

A/Contents: annotation; conformation by (1)H-NMR

C/Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynap

C/Superfamily: alpha-conotoxin

C/Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; blocked carboxyl e

F:1-15/Product: conotoxin GIA #status experimental <GRA>

F:1-13/Product: conotoxin GI #status experimental <GIC>

2-7,3-13/Disulfide bonds: #link GIA #status predicted
 2-7,3-13/Disulfide bonds: #link GIC #status experimental
 13/Modified site: amidated carboxyl end (Cys) (amide in mature form from following cly
 15/Modified site: blocked carboxyl end (Lys) (probably amidated) #status experimental

Query Match 25.2%; Score 31; DB 1; Length 15;
 Best Local Similarity 50.0%; Pred. No. 4.2e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

6 CLIPACRRH 15
 2 CCNPACGRH 11

SULT 12

9045
 pha-conotoxin AuIB - cone shell (Conus aulicus)
 Species: Conus aulicus (Court cone)
 Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999
 Accession: B59045
 Neurosci. 18, 8571-8579, 1998
 Luo, S.; Kulak, J.M.; Cartier, G.E.; Jacobsen, R.B.; Yoshikami, D.; Olivera, B.M.; McI
 Title: Alpha-conotoxin AuIB selectively blocks alpha3beta4 nicotinic acetylcholine rec
 Reference number: A59045; MUID:99003392; PMID:9786965
 Accession: B59045
 Status: preliminary
 Molecule type: protein
 Residues: 1-15 <LUO>

Superfamily: alpha-conotoxin
 Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro
 1-15/Product: alpha-conotoxin AuIB #status experimental <MAT>
 2-8,3-15/Disulfide bonds: #status experimental
 15/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 24.4%; Score 30; DB 2; Length 15;
 Best Local Similarity 57.1%; Pred. No. 5.8e+02;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

5 CCLIPAC 11
 2 CCSPPC 8

SULT 13

8963
 pha-conotoxin CnIA - cone shell (Conus consors)
 Contains: alpha-conotoxin CnIB
 Species: Conus consors
 Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
 Accession: A58963
 Favreau, P.; Krimm, I.; Le Gall, F.; Bobenrieth, M.J.; Lamhanh, H.; Bouet, F.; Servet
 ochimistry 38, 6317-6326, 1999
 Title: Biochemical characterization and nuclear magnetic resonance structure of novel
 Reference number: A58963; MUID:99255390; PMID:10320362
 Accession: A58963
 Status: preliminary
 Molecule type: protein
 Residues: 1-14 <FAV>

Superfamily: alpha-conotoxin
 Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro
 1-14/Product: alpha-conotoxin CnIA #status experimental <MAT>
 3-14/Product: alpha-conotoxin CnIB #status experimental <MAT>
 3-8,4-14/Disulfide bonds: #status experimental
 14/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 24.0%; Score 29.5; DB 2; Length 14;
 Best Local Similarity 75.0%; Pred. No. 6.5e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

4 RCCLIPAC 11
 2 RCC-HPAC 8

RESULT 14

A53709
 alpha-conotoxin ImI - cone shell (Conus imperialis)
 N Alternate names: alpha-Ctx-ImI
 C Species: Conus imperialis (Imperial cone)
 C Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C Accession: A53709
 R McIntosh, J.M.; Yoshikami, D.; Mahe, E.; Nielsen, D.B.; Rivier, J.E.; Gray, W.R.; Oli
 J. Biol. Chem. 269, 16733-16739, 1994
 A Title: A nicotinic acetylcholine receptor ligand of unique specificity, alpha-conotox
 A Reference number: A53709; MUID:94266889; PMID:8206995
 A Accession: A53709
 A Molecule type: protein
 A Residues: 1-12 <MC>

A Note: structure confirmed by chemical synthesis
 C Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynap
 C Superfamily: alpha-conotoxin
 C Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro
 F 2-8,3-12/Disulfide bonds: #status experimental
 F 12/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 22.8%; Score 28; DB 1; Length 12;
 Best Local Similarity 57.1%; Pred. No. 9.6e+02;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CCLIPAC 11
 DB 2 CCSPPC 8

RESULT 15

A54534
 heat-stable enterotoxin - Vibrio mimicus (fragment)
 C Species: Vibrio mimicus
 C Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 03-May-1996
 C Accession: A54534
 R Arita, M.; Honda, T.; Miwatani, T.; Takeda, T.; Takao, T.; Shimonishi, Y.
 FEMS Microbiol. Lett. 79, 105-110, 1991
 A Title: Purification and characterization of a heat-stable enterotoxin of Vibrio mimic
 A Reference number: A54534
 A Accession: A54534
 A Status: preliminary
 A Molecule type: protein
 A Residues: 1-17 <ARI>

C Superfamily: heat-stable enterotoxin ST
 Query Match 22.4%; Score 27.5; DB 2; Length 17;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 6; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 5 CCLIPAC 11
 DB 3 CCCLIPAC 12

RESULT 16

PH1781
 T cell receptor alpha chain V region (clone 2DN V alpha 24-2) - human (fragment)
 C Species: Homo sapiens (man)
 C Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
 C Accession: PH1781
 R Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
 J. Exp. Med. 178, 1-16, 1993
 A Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A Reference number: PH1754; MUID:93301585; PMID:8391057
 A Accession: PH1781
 A Status: preliminary
 A Molecule type: mRNA
 A Residues: 1-16 <POR>

Query Match 22.0%; Score 27; DB 2; Length 16;

Best Local Similarity 80.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

5 CCLIP 9
|||
6 CCLQP 10

SULT 22
1103
at-stable enterotoxin ST-1a - Citrobacter freundii
Species: Citrobacter freundii
Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 18-Jun-1993
Accession: A60103
Quarino, A.; Giannella, R.; Thompson, M.R.
fect. Immun. 57, 649-652, 1989
Title: Citrobacter freundii produces an 18-amino-acid heat-stable enterotoxin identical
Reference number: A60103; MUID:89108617; PMID:2912902
Accession: A60103
Molecule type: protein
Residues: 1-18 <GUA>
Superfamily: heat-stable enterotoxin ST

Query Match 20.7%; Score 25.5; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.9e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

5 CCLI---PAC 11
|||
5 CCELCNCPAC 14

SULT 23
8953
pha-conotoxin SI - cone shell (Conus striatus)
Species: Conus striatus (striated cone)
Date: 30-Jun-1989 #sequence_revision 25-Apr-1997 #text_change 23-May-1997
Accession: A28953
Zafaralla, G.C.; Ramilo, C.; Gray, W.R.; Karlstrom, R.; Olivera, B.M.; Cruz, L.J.
chemistry 27, 7102-7105, 1988
Title: Phylogenetic specificity of cholinergic ligands: alpha-conotoxin SI.
Reference number: A28953; MUID:89062448; PMID:3196703
Accession: A28953
Molecule type: protein
Residues: 1-13 <ZAP>
Note: This sequence was confirmed by chemical synthesis
Comment: This paralytic toxin from a fish-hunting cone snail inhibits the acetylcholin
Superfamily: alpha-conotoxin
Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro
2-7,3-13/Disulfide bonds: #status experimental
13/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 20.3%; Score 25; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 2.7e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

6 CLIPAC 11
|||
2 CCNPAC 7

SULT 24
14823
factory receptor I7 - mouse (fragment)
Species: Mus musculus (house mouse)
Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
Accession: A54823
Chess, A.; Simon, I.; Cedar, H.; Axel, R.
ll 78, 823-834, 1994
Title: Allelic inactivation regulates olfactory receptor gene expression.
Reference number: A54823; MUID:94373818; PMID:8087849
Accession: A54823
Status: Preliminary

A;Molecule type: DNA
A;Residues: 1-8 <CHE>

Query Match 19.5%; Score 24; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 RRNH 15
|||
3 RRNH 6

DB 3 RRNH 6

RESULT 25
B54823
olfactory receptor I7 - western wild mouse (fragment)
C;Species: Mus spretus (western wild mouse)
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
C;Accession: B54823
R;Chess, A.; Simon, I.; Cedar, H.; Axel, R.
Cell 78, 823-834, 1994
A;Title: Allelic inactivation regulates olfactory receptor gene expression.
A;Reference number: A54823; MUID:94373818; PMID:8087849
A;Accession: B54823
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-8 <CHE>

Query Match 19.5%; Score 24; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 RRNH 15
|||
3 RRNH 6

DB 3 RRNH 6

RESULT 26
S61797
T-cell-specific transcription factor 1 splice form F - human (fragment)
N;Alternate names: transcription factor TCF-1F
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 24-Jul-1998
C;Accession: S61797; S61879
R;Mayer, K.; Wolff, E.; Clevers, H.; Ballhausen, W.G.
Biochim. Biophys. Acta 1263, 169-172, 1995
A;Title: The human high mobility group (HMG)-box transcription factor TCF-1: novel iso
A;Reference number: S61796; MUID:95367594; PMID:7640309
A;Accession: S61797
A;Molecule type: mRNA
A;Residues: 1-11 <WAY>
A;Cross-references: EMBL:Z47363
A;Note: DNA was also sequenced
C;Keywords: alternative splicing; DNA binding; transcription factor

Query Match 19.5%; Score 24; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 IPAC 11
|||
3 IPAC 6

DB 3 IPAC 6

RESULT 27
A58700
actgadinine [validated] - "Actinoplanes liguriae"
N;Alternate names: gardimycin
C;Species: "Actinoplanes liguriae"
A;Note: ATCC 31048
C;Date: 16-Jan-1998 #sequence_revision 23-Jan-1998 #text_change 15-Sep-2000
C;Accession: A58700; A58701
R;Zimmermann, N.; Jung, G.
Eur. J. Biochem. 246, 809-819, 1997

Title: The three-dimensional solution structure of the lantibiotic murein-biosynthesis reference number: A58700; MUID:97363218; PMID:9219543
 Accession: A58700
 Molecule type: protein
 Residues: 1-19 <ZIM>
 Note: the assignment of residues 1-Ser and 6-Cys are based on model studies
 Zimmermann, N.; Metzger, J.W.; Jung, G.
 J. Biochem. 228, 786-797, 1995
 Title: The tetracyclic lantibiotic actagardine. (1)H-NMR and (13)C-NMR assignments and reference number: A58701; MUID:95255286; PMID:7737178
 Accession: A58701
 Molecule type: protein
 Residues: X, 2-5, X', 7-19 <Z12>
 Note: residues 1 and 6, indicated as 'X', are serine and cysteine, but which is in which
 Zimmermann, N.; Jung, G.
 Submitted to the Brookhaven Protein Data Bank, May 1997
 Reference number: A67976; PDB:1AJ1
 Contents: annotation, conformation and cross-link assignments by (1)H- and (13)C-NMR, comment: the antibiotic activity arises through inhibition of a glycopeptide transglycosylase
 Superfamily: unassigned lantionine-containing peptides
 Keywords: antibiotic; lantionine
 L-6/Cross-link: sn-(2S,6R)-lantionine (Ser-Cys) #status experimental
 7-12/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Thr-Cys) #status experimental
 9-17/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Thr-Cys) #status experimental
 14-19/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Thr-Cys) #status experimental
 Query Match 19.5%; Score 24; DB 2; Length 19;
 Best Local Similarity 44.4%; Pred. No. 4.9e+03;
 Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 3 WRCCLIPAC 11
 4 WVCITIEC 12
 3495
 noprassin S - cone shell (Conus striatus)
 Alternate names: Arg-vasopressin-S
 Species: Conus striatus (striated cone)
 Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 25-Apr-1997
 Accession: B28495
 Cruz, L.J.; de Santos, V.; Zafaralla, G.C.; Ramilo, C.A.; Zeikus, R.; Gray, W.R.; Oliver, B.L.
 Biochem. 262, 15921-15924, 1997
 Title: Invertebrate vasopressin/oxytocin homologs. Characterization of peptides from Conus striatus
 Reference number: A92617; MUID:88058932; PMID:3680228
 Accession: B28495
 Molecule type: protein
 Residues: 1-9 <CRU>
 Superfamily: oxytocin-neurophysin
 Keywords: amidated carboxyl end; venom
 1-6/Disulfide bonds: #status experimental
 9/Modified site: amidated carboxyl end (Gly) #status experimental
 Query Match 18.7%; Score 23; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 6 CLIPACRR 13
 1 CTRNCP 8
 6383
 pothetical protein - soybean
 Species: Glycine max (soybean)
 Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-May-2000
 Accession: T06383
 Dewey, R.E.; Wilson, R.F.; Novitzky, W.P.; Goode, J.H.
 Ant Cell 6, 1495-1507, 1994
 Title: The AAP1 gene of soybean complements a cholinephosphotransferase-deficient mutant
 Reference number: Z06169; MUID:95086383; PMID:7994181

A/Accession: T06383
 A/Status: preliminary; translated from GB/EMBL/DDBJ
 A/Molecule type: mRNA
 A/Residues: 1-11 <DEW>
 A/Cross-references: EMBL:U12735; NID:9530086; PIDN:AAA67718.1; PID:9530087
 A/Experimental source: strain Dare; seed
 Query Match 18.7%; Score 23; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 RCC 6
 DB 5 RCC 7
 RESULT 30
 B32800
 hypothetical protein (P1 5' region) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 30-Sep-1993
 C/Accession: B32800
 R.Jindal, S.; Dudani, A.K.; Singh, B.; Harley, C.B.; Gupta, R.S.
 Mol. Cell. Biol. 9, 2279-2283, 1989
 A/Title: Primary structure of a human mitochondrial protein homologous to the bacterial
 A/Reference number: A32800; MUID:89313783; PMID:2568584
 A/Accession: B32800
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-15 <JIN>
 A/Cross-references: GB:M22382
 Query Match 18.7%; Score 23; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 ACRR 13
 DB 9 ACRR 12
 RESULT 31
 PC1324
 hypothetical protein 19 - curled-leaved tobacco chloroplast (fragment)
 C/Species: chloroplast Nicotiana glauca (curled-leaved tobacco)
 C/Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 24-Feb-1995
 C/Accession: PC1324
 R.Pejes, E.; Engler, D.; Maliga, P.
 Theor. Appl. Genet. 79, 28-32, 1990
 A/Title: Extensive homologous chloroplast DNA recombination in the pt14 Nicotiana somat
 A/Reference number: PC1321
 A/Accession: PC1324
 A/Molecule type: DNA
 A/Residues: 1-19 <FEJ>
 C/Genetics:
 A/Genome: chloroplast
 C/Keywords: chloroplast
 Query Match 18.7%; Score 23; DB 2; Length 19;
 Best Local Similarity 50.0%; Pred. No. 6.8e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 9 PACRRNHK 16
 DB 1 PGRRRNYQ 8
 RESULT 32
 PC1322
 hypothetical protein 19 - common tobacco chloroplast (fragment)
 C/Species: chloroplast Nicotiana glauca (common tobacco)
 C/Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 24-Feb-1995
 C/Accession: PC1322

Fejes, E.; Engler, D.; Maliga, P.
 J. Appl. Genet. 79, 28-32, 1990
 Title: Extensive homologous chloroplast DNA recombination in the ptl4 Nicotiana somati-
 cus mutant
 Reference number: PC1321

Accession: PC1322
 Molecule type: DNA
 Residues: 1-19 <FEJ>
 Genomics:
 Genome: chloroplast
 Keywords: chloroplast

Query Match 18.7%; Score 23; DB 2; Length 19;
 Best Local Similarity 50.0%; Pred. No. 6.8e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

9 PACRRNHK 16

1 PGRRRNYQ 8

SULT 33

nganese peroxidase (EC 1.11.1.13) MnPI - Pleurotus eryngii (fragment)

Species: Pleurotus eryngii
 Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 29-Aug-1997

Accession: S65435
 Martinez, M.J.; Ruiz-Duenas, F.J.; Guillen, F.; Martinez, A.T.

x J. Biochem. 237, 424-432, 1996

Title: Purification and catalytic properties of two manganese peroxidase isoenzymes fr
 Reference number: S65434; MUID:96215438; PMID:8647081

Accession: S65435

Molecule type: protein

Residues: 1-19 <MAR>

Experimental source: CBS 613.91

Keywords: manganese; oxidoreductase

Query Match 18.7%; Score 23; DB 2; Length 19;

Best Local Similarity 42.9%; Pred. No. 6.8e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

2 NWRCCLI 8

11 NAACCVL 17

RESULT 34

ane Cfr protein - mouse (fragment)

Species: Mus sp. (mouse)

Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 28-Feb-1997

Accession: I57018

Dorin, J.K.; Stevenson, B.J.; Fleming, S.; Alton, E.W.; Dickinson, P.; Porteous, D.J.

Imm. Genome 5, 465-472, 1994

Title: Long-term survival of the exon 10 insertional cystic fibrosis mutant mouse is a
 Reference number: I57018; MUID:95037043; PMID:7949729

Accession: I57018

Status: preliminary; translated from GB/EMBL/DBJ

Molecule type: DNA

Residues: 1-8 <RES>

Cross-references: GB:S74246; NID:g710482

Genetics:

Gene: Cfr

Query Match 17.9%; Score 22; DB 2; Length 8;

Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

9 PACR 12

5 PSOR 8

RESULT 35

I49637
 deoxynucleotidyltransferase - mouse (fragment)
 Species: Mus musculus (house mouse)
 Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
 Accession: I49637
 R;Koizumi, O.; Kaneda, T.; Morishita, R.
 Biochem. Biophys. Res. Commun. 144, 185-190, 1987
 Title: Analysis of human terminal deoxynucleotidyl transferase cDNA expressible in ma
 Reference number: I45884; MUID:87213162; PMID:3579900
 Accession: I49637
 Status: preliminary; translated from GB/EMBL/DBJ
 Molecule type: mRNA
 Residues: 1-13 <RES>
 Cross-references: GB:M26145; NID:g951208; PIDN:AAA74592.1; PID:g951209
 Genetics:
 Gene: DNTT

Query Match 17.9%; Score 22; DB 2; Length 13;
 Best Local Similarity 75.0%; Pred. No. 7.2e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CLIP 9

DB 8 CLIP 11

Search completed: February 18, 2004, 06:29:21
 Job time : 22 secs

result No.	Score	Query			ID	Description
		Match	Length	DB		
1	123	100.0	19	1	CXA CONTU	P58911 conus tulip
2	48	39.0	16	1	CXAÅ CONPE	P50984 conus penna
3	44	35.8	16	1	CXA1 CONEP	P56638 conus episc
4	44	33.8	16	1	CXA2 CONMA	P56636 conus magus
5	42	34.1	16	1	CXA8 CONPE	P50985 conus penna
6	42	34.1	16	1	CXA1 CONER	P50982 conus ermin
7	38	32.5	18	1	CXA1 CONAL	P56639 conus aulic
8	37.5	30.5	14	1	CXA1 CONMA	P01521 conus magus
9	37	30.1	16	1	CXA3 CONAL	P56641 conus aulic
10	31	25.2	13	1	CXA4 CONST	P28878 conus stria
11	31	25.2	15	1	CXA1 CONGE	P01519 conus geogr
12	30	24.4	15	1	CXA2 CONAL	P56640 conus aulic
13	29.5	24.0	14	1	CXA1 CONCN	P56973 conus conso
14	28	22.8	12	1	CXA1 CONIM	P50983 conus imper
15	27	22.0	8	1	CSW2 CONPU	P58785 conus purpu
16	27	22.0	18	1	HSTB ECOLI	P01560 escherichia
17	26	21.1	9	1	DNF1 LOCM1	P16339 locusta mig
18	26	21.1	13	1	CXA2 CONGE	P01520 conus geogr
19	26	21.1	15	1	CX3B CONQU	P58842 conus geogr
20	25	20.3	17	1	CXMA CONPE	P58926 conus penna
21	24	19.5	15	1	CX1B CONBE	P58624 conus betul
22	24	19.5	15	1	CX3A CONQU	P58941 conus geogr
23	24	19.5	17	1	CXMB CONPE	P58927 conus penna
24	24	19.5	19	1	LANA ACTUG	P58650 actinoplanes
25	24	19.5	19	1	LCPR PETMA	Q10996 petromyzon
26	23	18.7	9	1	CONO CONST	P05487 conus stria
27	23	18.7	12	1	CX13 CONNR	P58809 conus marmo
28	23	18.7	18	1	LVC ESTAC	P82175 estigmenes a
29	22	17.9	10	1	GON2 CHERP	P80578 chelyosoma
30	22	17.9	11	1	TIN1 HOPI1	P82851 hapiobatrach
31	22	17.9	15	1	AVP2 CAVPO	P83508 cavia porce
32	22	17.9	15	1	UC08 MAIZE	P80614 zea mays (m
33	21	17.1	19	1	OXYT BUFRP	P42995 bufo regula

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CXAA_CONPE STANDARD; PRT; 16 AA.
P50984;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alpha-conotoxin PnIA.
Conus pennaceus (Feathered cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=37335;
[1]
SEQUENCE.
TISSUE=Venom;
MEDLINE=94347713; PubMed=8068627;
Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D.,
Spira M.E., Zlotkin E.;
"New mollusc-specific alpha-conotoxins block Aplysia neuronal
acetylcholine receptors.";
Biochemistry 33:9523-9529(1994).
[2]
SULFATION OF TYR-15.
MEDLINE=99242956; PubMed=10226369;
Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M.,
Baldwin M.A., Burlingame A.L.;
"Identification of tyrosine sulfation in Conus pennaceus conotoxins
alpha-PnIA and alpha-PnIB: further investigation of labile sulfo- and
phosphopeptides by electrospray, matrix-assisted laser desorption/ionization (MALDI) and atmospheric pressure MALDI mass
spectrometry.";
J. Mass Spectrom. 34:447-454(1999).
[3]
X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
MEDLINE=96311277; PubMed=8740364;
Hu S.-H., Gehrmann J., Guddat L.W., Alewood P.F., Craik D.J.,
Martin J.L.;
"The 1.1 A crystal structure of the neuronal acetylcholine receptor
antagonist, alpha-conotoxin PnIA from Conus pennaceus.";
Structure 4:417-423(1996).
-!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
bind to the nicotinic acetylcholine receptors (nAChR) and thus
inhibit them. In contrast to other alpha-conotoxins, which are
selective for vertebrate skeletal muscle nAChR, the Conus
pennaceus alpha-conotoxins block nAChR in mollusks.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom duct.
-!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
family.
PIR; A54877; A54877.
PDB; 1FEN; 21-APR-97.
Postsynaptic neurotoxin; Neurotoxin; Toxin;
Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.
DISULFID 2 8
MOD_RES 3 16 SULFATION.
MOD_RES 15 15 AMIDATION.
HELI 2 4
HELI 6 11
TURN 13 16
SEQUENCE 16 AA; 1628 MW; 05310FF95EC99005 CRC64;
Query Match 39.0%; Score 48; DB 1; Length 16;
Best Local Similarity 40.0%; Pred. No. 0.26;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
Y 5 CCLIPACRRNHKKFC 19
||| | | | | |
b 2 CGLPPCAANNPDYC 16
[1]
SEQUENCE, AND SYNTHESIS.
RC TISSUE=Venom;
RA MEDLINE=96205934; PubMed=8631783;
RA Cartier G.E., Yoshikami D., Gray W.R., Luo S., Olivera B.M.,
RA McIntosh J.M.;
" A new alpha-conotoxin which targets alpha3beta2 nicotinic
acetylcholine receptors.";
RL J. Biol. Chem. 271:7522-7528(1996).
[2]
RESULT 3
XAL_CONEP STANDARD; PRT; 16 AA.
D CXAL_CONEP
CXAA2_CONVA STANDARD; PRT; 16 AA.
AC P56636;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-conotoxin MII (M2).
OS Conus magus (Magus cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=6492;
[1]
SEQUENCE, AND SYNTHESIS.
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Venom;
RA MEDLINE=96205934; PubMed=8631783;
RA Cartier G.E., Yoshikami D., Gray W.R., Luo S., Olivera B.M.,
RA McIntosh J.M.;
" A new alpha-conotoxin which targets alpha3beta2 nicotinic
acetylcholine receptors.";
RL J. Biol. Chem. 271:7522-7528(1996).
[2]

```

STRUCTURE BY NMR.
MEDLINE=98062282; PubMed=9398298;
Shon K.-J., Koerber S.C., Rivier J.B., Olivera B.M., McIntosh J.M.;
"Three-dimensional solution structure of alpha-conotoxin MII, an
alpha3beta2 neuronal nicotinic acetylcholine receptor-targeted
ligand.";
Biochemistry 36:15693-15700(1997).
[3]

STRUCTURE BY NMR.
MEDLINE=99060038; PubMed=9843366;
Hill J.M., Omen C.J., Miranda L.P., Bingham J.-P., Alewood P.P.,
Craik D.J.;
"Three-dimensional solution structure of alpha-conotoxin MII by NMR
spectroscopy: effects of solution environment on helicity.";
Biochemistry 37:15621-15630(1998).

-!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
bind to the nicotinic acetylcholine receptors (nAChR) and thus
inhibit them. This peptide blocks mammalian nicotinic
acetylcholine receptors composed of alpha-3/beta-2 subunits. It
has an activity 2 to 4 orders of magnitude less potent on other
nAChR subunit combinations.

-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom duct.
-!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
family.

PIR; A59046; A59046.
PDB; 1MI1; 21-OCT-98.
PDB; 1M2C; 13-JAN-99.
Postsynaptic neurotoxin; Neurotoxin; Toxin;
Acetylcholine receptor inhibitor; Amidation; 3D-structure.

DISULFID 2 8
DISULFID 3 16
MOD_RES 16 16
TURN 2 4
HELI 7 11
TURN 12 16

SEQUENCE 16 AA; 1716 MW; 282AEF190166CAF9 CRC64;

Query Match 35.8%; Score 44; DB 1; Length 16;
Best Local Similarity 40.0%; Pred. No. 1;
Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19
|||:|:|:|:|:|:|:
2 CCSNPVCHLEHNSLC 16

SULT 5
AB_CONPE STANDARD; PRT; 16 AA.
P50983;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alpha-conotoxin PnIB.
Conus pennaceus (Feathered cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=37335;
[1]
SEQUENCE.

TISSUE=Venom;
MEDLINE=94347719; PubMed=8068627;
Fainzilber M., Hesson A., Oren R., Burlingame A.L., Gordon D.,
Spira M.E., Zlotkin E.;
"New mollusc-specific alpha-conotoxins block Aplysia neuronal
acetylcholine receptors.";
Biochemistry 33:9523-9529(1994).
[2]

SULFATION OF TYR-15.
MEDLINE=99242956; PubMed=10226369;
Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M.,

RA Baldwin M.A., Burlingame A.L.;
"Identification of tyrosine sulfation in Conus pennaceus conotoxins
RT alpha-PnIA and alpha-PnIB: further investigation of labile sulfo- and
RT phosphopeptides by electrospray matrix-assisted laser
RT desorption/ionization (MALDI) and atmospheric pressure MALDI mass
RT spectrometry.";
RL J. Mass Spectrom. 34:447-454 (1999).
RN [3]

RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
RX MEDLINE=97444322; PubMed=9298951;
RA Hu S.H., Gehrmann J., Alewood P.P., Craik D.J., Martin J.L.;
RT "Crystal structure at 1.1-A resolution of alpha-conotoxin PnIB:
RL comparison with alpha-conotoxins PnIA and Gi.";
RL Biochemistry 36:11323-11330(1997).

CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
bind to the nicotinic acetylcholine receptors (nAChR) and thus
inhibit them. In contrast to other alpha-conotoxins, which are
selective for vertebrate skeletal muscle nAChR, the Conus
pennaceus alpha-conotoxins block nAChR in mollusks.

CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
family.

PIR; B54877; B54877.
PDB; 1AKG; 20-MAY-98.
Postsynaptic neurotoxin; Neurotoxin; Toxin;
Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.

DISULFID 2 8
DISULFID 3 16
MOD_RES 15 15
FT MOD_RES 16 16
FT AMIDATION.

FT HELIX 2 4
FT HELIX 6 11
FT TURN 13 16
SEQUENCE 16 AA; 1643 MW; 05310FF95ED86AF5 CRC64;

Query Match 34.1%; Score 42; DB 1; Length 16;
Best Local Similarity 33.3%; Pred. No. 2;
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19
|||:|:|:|:|:|:|:
DB 2 CCSLPFCALSNPDYC 16

RESULT 6
CXAL_CONER STANDARD; PRT; 18 AA.
ID AC P50982;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-conotoxin EI.
OS Conus ermineus (Atlantic fish-hunting cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=55423;
RN [1]
RP SEQUENCE.

TISSUE=Venom;
MEDLINE=96062516; PubMed=7578057;
Martinez J.S., Olivera B.M., Gray W.R., Craig A.G., Groebe D.R.,
RA Abramson J.N., McIntosh J.M.;
RT "Alpha-conotoxin EI, a new nicotinic acetylcholine receptor
RT antagonist with novel selectivity.";
RL Biochemistry 34:14519-14526(1995).

CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
bind to the nicotinic acetylcholine receptors (nAChR) and thus
inhibit them.
CC -!- SUBUNIT: Binds nicotinic acetylcholine receptor.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.

-1- SUBCELLULAR LOCATION: Secreted.
 -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 -1- MASS SPECTROMETRY: MW=1667.6; METHOD=Electrospray.
 -1- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type family.

PIR: CS9045, CS9045.
 HSPSP: P50984, 1PEN.
 Postsynaptic neurotoxin; Neurotoxin; Toxin;
 Acetylcholine receptor inhibitor; Amidation.
 DISULFID 2 8
 MOD_RES 3 16
 SEQUENCE 16 AA; 1673 MW; 1E310D3B9FDC7001 CRC64;

Query Match 30.1%; Score 37; DB 1; Length 16;
 Best Local Similarity 33.3%; Pred. No. 11;
 Matches 5; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19
 ||||| : : :
 2 CCSYPFCFATNSGYC 16

SULT 10

AA_CONGE STANDARD; PRT; 13 AA.
 P28878; 01-DEC-1992 (Rel. 24, Created)
 01-DEC-1992 (Rel. 24, Last sequence update)
 28-FEB-2003 (Rel. 41, Last annotation update)
 Alpha-conotoxin SIA (S1A).
 Conus striatus (Striated cone).
 Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 Neogastropoda; Conoidea; Conidae; Conus.
 NCBI_TaxID=6493;
 [1]
 SEQUENCE.
 TISSUE=Venom;
 MEDLINE=91369955; PubMed=1892838;
 Myers R.A., Zafarella G.C., Gray W.R., Abbot J., Cruz L.J.,
 Olivera B.M.;
 "Alpha-conotoxins, small peptide probes of nicotinic acetylcholine receptors."
 Biochemistry 30:9370-9377(1991).
 -1- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they bind to the nicotinic acetylcholine receptors (nAChR) and thus inhibit them.
 -1- SUBCELLULAR LOCATION: Secreted.
 -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 -1- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type family.

PIR: A40312; NTKNAS.
 Postsynaptic neurotoxin; Neurotoxin; Toxin;
 Acetylcholine receptor inhibitor; Amidation.
 DISULFID 2 7
 MOD_RES 3 13
 SEQUENCE 13 AA; 1461 MW; DEF1931982457EBD CRC64;

Query Match 25.2%; Score 31; DB 1; Length 13;
 Best Local Similarity 55.6%; Pred. No. 70;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

6 CCLIPACRRNH 14
 ||||| : : :
 2 CCHPACGCKN 10

ISULT 11

AA_CONGE STANDARD; PRT; 15 AA.
 P01519;

DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Alpha-conotoxin GIA [Contains: Alpha-conotoxin GI (GI)].
 OS Conus geographus (Geography cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 CX NCBI_TaxID=6491;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=81191854; PubMed=7014556;
 RA Gray W.R., Lucue F.A., Olivera B.M., Barrett J., Cruz L.J.;
 "Peptide toxins from Conus geographus venom."
 J. Biol. Chem. 256:4734-4740(1981).
 RN [2]
 RP DISULFIDE BONDS OF GI, AND SYNTHESIS OF GI.
 RX MEDLINE=83105694; PubMed=7152021;
 RA Nishiuchi Y., Sakakibara S.;
 "Primary and secondary structure of conotoxin GI, a neurotoxic tridecapeptide from a marine snail."
 FEBS Lett. 148:260-262(1982).
 RN [3]
 RP DISULFIDE BONDS OF GI, AND SYNTHESIS OF GI.
 RX MEDLINE=84280842; PubMed=6466616;
 RA Gray W.R., Lucue F.A., Galyean R., Atherton E., Sheppard R.C.,
 Stone B.L., Reyes A., Alford J., McIntosh M., Olivera B.M.,
 Cruz L.J., Rivier J.;
 "Conotoxin GI: disulfide bridges, synthesis, and preparation of iodinated derivatives."
 Biochemistry 23:2796-2802(1984).
 RN [4]
 RP COMPARISON WITH ALPHA-CONOTOXIN SI AND ALPHA-CONOTOXIN MI.
 RX MEDLINE=95034849; PubMed=7947815;
 RA Hann R.M., Pagan O.R., Eterovic V.A.;
 "The alpha-conotoxins GI and MI distinguish between the nicotinic acetylcholine receptor agonist sites while SI does not."
 Biochemistry 33:14058-14063(1994).
 RN [5]
 RP PHARMACOLOGICAL CHARACTERIZATION ON MOUSE MUSCLE-DERIVED BC3H-1 CELLS AND TORPEDO ELECTRIC ORGAN.
 RX MEDLINE=95349531; PubMed=7623764;
 RA Groebe D.R., Dumm J.M., Levitan E.S., Abramson S.N.;
 "alpha-Conotoxins selectively inhibit one of the two acetylcholine binding sites of nicotinic receptors."
 Mol. Pharmacol. 48:105-111(1995).
 RN [6]
 RP MUTAGENESIS OF ARG-9.
 RX MEDLINE=97317090; PubMed=9174364;
 RA Groebe D.R., Gray W.R., Abramson S.N.;
 "Determinants involved in the affinity of alpha-conotoxins GI and SI for the muscle subtype of nicotinic acetylcholine receptors."
 Biochemistry 36:6469-6474(1997).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (1.2 ANGSTROMS) OF GI.
 RX MEDLINE=96378624; PubMed=8784187;
 RA Guddat L.W., Martin J.A., Shan L., Edmundson A.B., Gray W.R.;
 "Three-dimensional structure of the alpha-conotoxin GI at 1.2-A resolution."
 Biochemistry 35:11329-11335(1996).
 RN [8]
 RP STRUCTURE BY NMR OF GI.
 RX MEDLINE=89352562; PubMed=2765514;
 RA Kobayashi Y., Ohkubo T., Kyogoku Y., Nishiuchi Y., Sakakibara S.,
 Braun W., Go N.;
 "Solution conformation of conotoxin GI determined by 1H nuclear magnetic resonance spectroscopy and distance geometry calculations."
 Biochemistry 28:4853-4860(1989).
 RN [9]
 RP STRUCTURE BY NMR OF GI.
 RX MEDLINE=89375269; PubMed=2775719;
 RA Pardi A., Galdes A., Florence J., Maniconte D.;
 "Solution structures of alpha-conotoxin GI determined by two-

RESULT 12
CXA2_CONAL
D_CXA2

Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 Neogastropoda; Conoidea; Conidae; Conus.
 NCBI_TaxID=101297;
 [1]
 SEQUENCE, SYNTHESIS, CHARACTERIZATION, AND STRUCTURE BY NMR.
 TISSUE=Venom;
 MEDLINE=92253390; PubMed=10320362;
 Favreau P., Krimm I., le Gall F., Bobenrieth M.J., Lamthanh H.,
 Bouet F., Servent D., Molgo J., Menez A., Letourneux Y.,
 Lancelin J.-M.;
 "Biochemical characterization and nuclear magnetic resonance
 structure of novel alpha-conotoxins isolated from the venom of Conus
 consors";
 Biochemistry 38:6317-6326(1999).
 -|- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
 bind to the nicotinic acetylcholine receptors (nAChR) and thus
 inhibit them. This peptide seems to be a potent and selective
 blocker of muscular subtype of nAChR.
 -|- SUBCELLULAR LOCATION: Secreted.
 -|- TISSUE SPECIFICITY: Expressed by the venom duct.
 -|- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
 family.
 PIR; A58963; A58963.
 PDB; 1B45; 09-JUL-99.
 Postsynaptic neurotoxin; Neurotoxin; Toxin;
 Acetylcholine receptor inhibitor; Amidation; 3D-structure.
 PEPTIDE 1 14
 1 14 ALPHA-CONOTOXIN CNIA.
 PEPTIDE 3 14
 3 8 DISULFID
 4 14
 14 14 AMIDATION.
 MOD RES 14 14
 6 8
 HELIX 5 10
 TURN 6 10
 SEQUENCE 14 AA; 1548 MW; DEEE1969BFE5E5D CRC64;
 Query Match 24.0%; Score 29.5; DB 1; Length 14;
 Best Local Similarity 75.0%; Pred. No. 1.2e-02;
 Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 4 RCCLIPAC 11
 |||||
 2 RCC-HPAC 8
 SULT 14.
 AL CONIM STANDARD; PRT; 12 AA.
 PS0983;
 01-OCT-1996 (Rel. 34, Created)
 01-OCT-1996 (Rel. 34, Last sequence update)
 28-FEB-2003 (Rel. 41, Last annotation update)
 Alpha-conotoxin Imi.
 Conus imperialis (Imperial cone).
 Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 Neogastropoda; Conoidea; Conidae; Conus.
 NCBI_TaxID=35631;
 [1]
 SEQUENCE, AND SYNTHESIS.
 TISSUE=Venom;
 MEDLINE=94266889; PubMed=8206995;
 McIntosh J.M., Yoshikami D., Mahe E., Nielsen D.B., Rivier J.E.,
 Gray W.R., Olivera B.M.;
 "A nicotinic acetylcholine receptor ligand of unique specificity,
 alpha-conotoxin Imi";
 J. Biol. Chem. 269:16733-16739(1994).
 [2]
 CHARACTERIZATION
 MEDLINE=95379776; PubMed=7651351;
 Jonsson D.S., Martinez J., Elgoyhen A.B., Heinemann S.F.,
 McIntosh J.M.;
 "Alpha-conotoxin Imi exhibits subtype-specific nicotinic

RT acetylcholine receptor blockade: preferential inhibition of homomeric
 RT alpha 7 and alpha 9 receptors.";
 RL Mol. Pharmacol. 48:194-199(1995).
 RN [3]
 RN STRUCTURE BY NMR.
 RX MEDLINE=99212205; PubMed=10194298;
 RA Rogers J.P., Luginbuhl P., Shen G.S., McCabe R.T., Stevens R.C.,
 RA Wemmer D.E.;
 "NMR solution structure of alpha-conotoxin Imi and comparison to
 RT other conotoxins specific for neuronal nicotinic acetylcholine
 RT receptors";
 RL Biochemistry 38:3874-3882(1999).
 RN [4]
 RN STRUCTURE BY NMR.
 RX MEDLINE=99280313; PubMed=10350614;
 RA Gouda H., Hirono S.;
 RT "Solution structure of alpha-conotoxin Imi determined by
 RT two-dimensional NMR spectroscopy";
 RL Biochim. Biophys. Acta 1431:384-394(1999).
 RN [5]
 RN STRUCTURE BY NMR.
 RX MEDLINE=99158061; PubMed=10050774;
 RA Maslemnikov I.V., Shenkarev Z.O., Zhmak M.N., Ivanov V.T.,
 RA Methfessel C., Tsetlin V.I., Arseniev A.S.;
 RT "NMR spatial structure of alpha-conotoxin Imi reveals a common
 RT scaffold in snail and snake toxins recognizing neuronal nicotinic
 RT acetylcholine receptors";
 RL FEBS Lett. 444:275-280(1999).
 RN [6]
 RN STRUCTURE BY NMR.
 RX MEDLINE=99358772; PubMed=10431825;
 RA Lamthanh H., Jegou-Matheron C., Servent D., Menez A., Lancelin J.-M.;
 RT "Minimal conformation of the alpha-conotoxin Imi for the alpha7
 RT neuronal nicotinic acetylcholine receptor recognition: correlated CD,
 RT NMR and binding studies";
 RL FEBS Lett. 454:293-298(1999).
 RN [7]
 RN STRUCTURE BY NMR.
 RX MEDLINE=99324017; PubMed=10395477;
 RA Gehrmann J., Daly N.L., Alewood P.F., Craik D.J.;
 RT "Solution structure of alpha-conotoxin Imi by 1H nuclear magnetic
 RT resonance";
 RL J. Med. Chem. 42:2364-2372(1999).
 RN [8]
 RN MUTAGENESIS OF ASP-5; ARG-7 AND ARG-11, AND STRUCTURE BY NMR OF THESE
 RN THREE MUTANTS.
 RX MEDLINE=20574023; PubMed=11124036;
 RA Rogers J.P., Luginbuhl P., Pemberton K., Harty P., Wemmer D.E.,
 RA Stevens R.C.;
 RT "Structure-activity relationships in a peptidic alpha7 nicotinic
 RT acetylcholine receptor antagonist";
 RL J. Mol. Biol. 304:911-926(2000).
 CC -|- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
 CC bind to the nicotinic acetylcholine receptors (nAChR) and thus
 CC inhibit them. It is highly active against the neuromuscular
 CC receptor in frog but not in mice. In contrast, it induces seizures
 CC when injected centrally in mice and rats. It targets neuronal
 CC nAChRs in mammals. It blocks homomeric alpha-7 nicotinic receptors
 CC with the highest apparent affinity and homomeric alpha-9 receptors
 CC with 8-fold lower affinity. It has no effect on receptors composed
 CC of alpha-2/beta-2, alpha-3/beta-2, alpha-4/beta-2, alpha-2/beta-4,
 CC alpha-3/beta-4, or alpha-4/beta-4 subunit combinations.
 CC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -|- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
 CC family.
 DR PIR; A53709; A53709.
 DR PDB; 1CNL; 27-MAY-99.
 DR PDB; 1E74; 27-DEC-00.
 DR PDB; 1E75; 27-DEC-00.
 DR PDB; 1E76; 27-DEC-00.
 DR PDB; 1G2G; 08-NOV-00.
 DR PDB; 1IM1; 15-JUN-99.


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PDB: 1IML; 23-APR-99.
Postsynaptic neurotoxin; Neurotoxin; Toxin;
Acetylcholine receptor inhibitor; Amidation; 3D-structure.
DISULFID 2 8
MOD RES 3 12
MUTAGEN 5 5
MUTAGEN 7 7
MUTAGEN 11 11
HELIX 2 4
TURN 10 12
SEQUENCE 12 AA; 1357 MW; 9C29CEAS45A4176A CRC64;
Query Match 22.8%; Score 28; DB 1; Length 12;
Best Local Similarity 57.1%; Pred. NO. 1.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

5 CCLIPAC 11
2 CCSDPRC 8

RESULT 15
W2_CONPU STANDARD; PRT; 8 AA.
P58785;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Leu-contryphan-P.
Conus purpurascens (Purple cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=411690;
[1]
SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
STRAIN=Clipperton Island; TISSUE=Venom;
MEDLINE=9338839; PubMed=10461743;
Jacobsen A.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
Oliviera B.M.;
"A novel D-leucine-containing Conus peptide: diverse conformational
dynamics in the contrypphan family.";
J. Pept. Res. 54:93-99(1999).
-1- SUBCELLULAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: Expressed by the venom duct.
-1- MASS SPECTROMETRY: MW=886.4; METHOD=LSIMS.
Toxin; Hydroxylation; D-amino acid.
DISULFID 2 4
MOD RES 4 4
D-LEUCINE.
SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;
Query Match 22.0%; Score 27; DB 1; Length 8;
Best Local Similarity 57.1%; Pred. NO. 1.4e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

5 CCLIPAC 11
2 CVLLPWC 8

RESULT 16
STB_ECOLI STANDARD; PRT; 18 AA.
P01560;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Heat-stable enterotoxin ST-2 (ST-B).
Escherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
SEQUENCE.
RC STRAIN=O42:K86:H37 / 18D;
RX MEDLINE=81264141; PubMed=7021541;
RA Chan S.-K., Giannella R.A.;
RT "Amino acid sequence of heat-stable enterotoxin produced by
Escherichia coli pathogenic for man.";
RL J. Biol. Chem. 255:7744-7746(1981).
RN [2]
RN DISULFIDE BONDS.
RX MEDLINE=87191003; PubMed=3552731;
RA Shimonishi Y., Hidaka Y., Koizumi M., Hane M., Aimoto S., Takeda T.,
Miwatani T., Takeda Y.;
RT "Mode of disulfide bond formation of a heat-stable enterotoxin (STh)
produced by a human strain of enterotoxigenic Escherichia coli.";
RL FEBS Lett. 215:165-170(1987).
CC -1- FUNCTION: TOXIN WHICH ACTIVATES THE PARTICULATE FORM OF GUANYLATE
CYCLASE AND INCREASES CYCLIC GMP LEVELS WITHIN THE HOST
INTESTINAL EPITHELIAL CELLS.
CC -1- DISEASE: BOTH HEAT-STABLE AND HEAT-LABILE ENTEROTOXINS ARE
PRODUCED BY PATHOGENIC STRAINS OF E.COLI AND AFFECT THE DIGESTIVE
TRACT OF MAMMALS.
CC -1- SIMILARITY: Belongs to the heat-stable enterotoxin family.
PIR; A01823; OHEC2.
DR HSPSP; P01559; 1ETN.
DR InterPro; IPR001489; Enterotoxin_HS.
DR Pfam; PF02048; Enterotoxin_HS; 1.
DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
KW Toxin; Enterotoxin.
FT DISULFID 5 10
FT DISULFID 6 14
FT DISULFID 9 17
SQ SEQUENCE 18 AA; 1978 MW; D0C975F49D500650 CRC64;
Query Match 22.0%; Score 27; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. NO. 3.7e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CLIPAC 11
DB 9 CCYPAC 14

RESULT 17
DNF1_LOCOMI STANDARD; PRT; 9 AA.
ID _DNF1_LOCOMI
AC P16339;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Locupressin (Diuretic neuropeptide F1/F2).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RN SEQUENCE.
RP TISSUE=Suboesophageal ganglion, and Thoracic ganglion;
RX MEDLINE=88077077; PubMed=3689410;
RA Proux J.P., Miller C.A., Li J.P., Carney R.L., Girardie A.,
Delaage M., Schooley D.A.;
RT "Identification of an arginine vasopressin-like diuretic hormone from
Locusta migratoria.";
RL Biochem. Biophys. Res. Commun. 149:180-186(1987).
CC -1- FUNCTION: DIURETIC HORMONE.
CC -1- SUBUNIT: Monomer (F1) and homodimer (F2); disulfide-linked.
CC -1- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR PIR; A29477; A29477.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.

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P59842;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Conotoxin QcIIIB.
Conus quercinus (Oak cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=101313;
[1]
SEQUENCE.
RP MEDLINE=90327072; PubMed=2165278;
RX Abogadie F.C., Ramilo C.A., Corpuz G.P., Cruz L.J.;
RRL Unpublished results, cited by:
RRL Olivera B.M., Rivier J.E., Clark C., Ramilo C.A., Corpuz G.P.,
RRL Abogadie F.C., Mena E.E., Woodward S.R., Hillyard D.R., Cruz L.J.;
RRL Science 249:257-263(1990).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: BELONGS TO THE M-SUPERFAMILY OF CONOTOXINS.
CC Toxin; Hydroxylation.
KW DISULFID 1 9 PROBABLE.
FT DISULFID 2 12 PROBABLE.
FT DISULFID 6 13 PROBABLE.
FT MOD_RES 11 11 HYDROXYLATION.
SQ SEQUENCE 15 AA; 1724 MW; C9CEBA917BED832D CRC64;

Query Match 21.1%; Score 26; DB 1; Length 15;
Best Local Similarity 55.6%; Pred. NO. 4.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

QY 3 WRCLLIIPAC 11
DB 7 WVC--IPCC 13

RESULT 20
CXNA_CONPE STANDARD; PRT; 17 AA.
ID CXNA_CONPE AC P58926;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mu-conotoxin PhIVA.
OS Conus pennaceus (Feathered cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OC NCBI_TaxID=37335;
RN [1]_SEQUENCE, AND MASS SPECTROMETRY.
RP MEDLINE=95337083; PubMed=7612605;
RX Fainzilber M., Nakamura T., Gaothon A., Loddner J.C., Kits K.S.,
RA Burlingame A.L., Zlotkin E.;
RT "A new cysteine framework in sodium
RT Biochemistry 34:8649-8656(1995).
CC -!- FUNCTION: Mu-conotoxins bind and block voltage-sensitive sodium
CC channel. Blocks reversibly sodium currents in bivalve mollusks
CC but has no effect on sodium currents in rat brain synaptosomes.
CC in rat brain synaptosomes. Induces paralysis in fish (Gambusia) and fly
CC (Mytilus). No effect are observed on sodium currents in molluscan neurons,
CC larvae (Sarcophaga). PhIVA is approximately 6 times more potent
CC than PhIVA in blockade of the sodium current in *Lymanaea* neurons.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=1789.5; METHOD=LSIMS.
CC -!- SIMILARITY: BELONGS TO THE M-SUPERFAMILY OF CONOTOXINS. MU-TYPE
CC FAMILY.
CC Toxin; Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor.
KW SITE 4 4 IMPORTANT FOR BINDING AND ACTIVITY.
FT DISULFID 1 12 BY SIMILARITY.
FT DISULFID 2 15 BY SIMILARITY.

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1  DISULFID 8 17 BY SIMILARITY
2  SEQUENCE 17 AA; 1757 MW; F9B721E0E96B9D82 CRC64;
3
4  Query Match 20.3%; Score 25; DB 1; Length 17;
5  Best Local Similarity 42.9%; Pred. No. 6.9e+02;
6  Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
7
8  1 FNRWCCL 7
9  : |||
10 4 YGWTCLL 10
11
12 RESULT 21
13 1B CONBE STANDARD; PRT; 15 AA.
14 58624;
15 28-FEB-2003 (Rel. 41, Created)
16 28-FEB-2003 (Rel. 41, Last sequence update)
17 28-FEB-2003 (Rel. 41, Last annotation update)
18 Conotoxin BetX1b.
19 Conus betulinus (Beech cone).
20 Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
21 Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
22 Neogastropoda; Conoidea; Conidae; Conus.
23 NCBI_TaxID=89764;
24 [1]
25 SEQUENCE, AND MASS SPECTROMETRY.
26 TISSUE=Venom;
27 MEDLINE=20059566; PubMed=10591037;
28 Chen J.-S., Fan C.-X., Hu K.-P., Wei K.-H., Zhong M.-N.;
29 "Studies on conotoxins of Conus betulinus.";
30 J. Nat. Toxins 8:341-349(1999).
31 -!- SUBCELLULAR LOCATION: Secreted.
32 -!- TISSUE SPECIFICITY: Expressed by the venom duct.
33 -!- MASS SPECTROMETRY: MW=1642.5; METHOD=MALDI.
34 -!- SIMILARITY: BELONGS TO THE M-SUPERFAMILY OF CONOTOXINS.
35 Neurotoxin; Toxin. 9 PROBABLE.
36 DISULFID 1 9
37 DISULFID 2 12 PROBABLE.
38 DISULFID 6 13 PROBABLE.
39 SEQUENCE 15 AA; 1650 MW; 3749B4F08E311337 CRC64;
40
41 Query Match 19.5%; Score 24; DB 1; Length 15;
42 Best Local Similarity 60.0%; Pred. No. 8.6e+02;
43 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
44
45 5 CCLIP 9
46 : |||
47 1 CCELP 5
48
49 RESULT 22
50 X3A CONQU STANDARD; PRT; 15 AA.
51 58841;
52 28-FEB-2003 (Rel. 41, Created)
53 28-FEB-2003 (Rel. 41, Last sequence update)
54 28-FEB-2003 (Rel. 41, Last annotation update)
55 Conotoxin Oc11a.
56 Conus guericus (Oak cone).
57 Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
58 Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
59 Neogastropoda; Conoidea; Conidae; Conus.
60 NCBI_TaxID=101313;
61 [1]
62 SEQUENCE.
63 MEDLINE=90327072; PubMed=2165278;
64 Abogadie F.C., Ramilo C.A., Corpuz G.P., Cruz L.J.;
65 Unpublished results, cited by:
66 Olivera B.M., Rivier J.E., Clark C., Ramilo C.A., Corpuz G.P.,
67 Abogadie F.C., Mera E.E., Woodward S.R., Hillyard D.R., Cruz L.J.;
68 Science 249:257-263(1990).
69 -!- FUNCTION: Causes scratching in mice.
70
71 CC -!- SUBCELLULAR LOCATION: Secreted.
72 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
73 CC -!- SIMILARITY: BELONGS TO THE M-SUPERFAMILY OF CONOTOXINS.
74 KW Toxin; Hydroxylation; Amidation.
75 FT DISULFID 1 9 PROBABLE.
76 FT DISULFID 2 12 PROBABLE.
77 FT DISULFID 6 13 PROBABLE.
78 FT MOD_RES 11 11 HYDROXYLATION.
79 FT MOD_RES 15 15 AMIDATION.
80 SQ SEQUENCE 15 AA; 1601 MW; D479B5AEB4ED832D CRC64;
81
82 Query Match 19.5%; Score 24; DB 1; Length 15;
83 Best Local Similarity 38.5%; Pred. No. 8.6e+02;
84 Matches 5; Conservative 0; Mismatches 2; Indels 6; Gaps 1;
85
86 QY 5 CC-----LIPAC 11
87 : |||
88 Db 1 CCSQDCLVCIPCC 13
89
90 RESULT 23
91 CXMB CONPE STANDARD; PRT; 17 AA.
92 AC P58927;
93 28-FEB-2003 (Rel. 41, Created)
94 DT 28-FEB-2003 (Rel. 41, Last sequence update)
95 DT 28-FEB-2003 (Rel. 41, Last annotation update)
96 DE Mu-conotoxin Pn1bV.
97 OS Conus pennaceus (Feathered cone).
98 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
99 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
100 OC Neogastropoda; Conoidea; Conidae; Conus.
101 OK NCBI_TaxID=37335;
102 [1]
103 RN SEQUENCE, AND MASS SPECTROMETRY.
104 RP MEDLINE=95337083; PubMed=7612605;
105 RA Fainzilber M., Nakamura T., Gaathon A., Lodder J.C., Kits K.S.,
106 Burlingame A.L., Zlotkin E.;
107 "A new cysteine framework in sodium channel blocking conotoxins.";
108 J. Biochemistry 34:8649-8656(1995).
109 [2]
110 RN PHARMACOLOGICAL CHARACTERIZATION.
111 RP MEDLINE=95346025; PubMed=7620628;
112 RA Haeson A., Fainzilber M., Zlotkin E., Spira M.E.;
113 "Electrophysiological characterization of a novel conotoxin that
114 blocks molluscan sodium channels.";
115 RL Eur. J. Neurosci. 7:815-818(1995).
116 CC -!- FUNCTION: Mu-conotoxins bind and block voltage-sensitive sodium
117 channel. Blocks reversibly sodium channels in molluscan neurons,
118 but has no effect on sodium currents in bovine chromaffin cells or
119 in rat brain synaptosomes. Induces paralysis in bivalve mollusks
120 (Mytilus). No effect are observed on fish (Gambusia) and fly
121 larvae (Sarcophaga). Is approximately 6 times more potent than
122 Pn1bV in blockade of the sodium current in Lymnaea neurons.
123 CC -!- SUBCELLULAR LOCATION: Secreted.
124 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
125 CC -!- MASS SPECTROMETRY: MW=1862.8; METHOD=LSIMS.
126 CC -!- SIMILARITY: BELONGS TO THE M-SUPERFAMILY OF CONOTOXINS. MU-TYPE
127 FAMILY.
128 KW Toxin; Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor.
129 FT SITE 4 4 IMPORTANT FOR BINDING AND ACTIVITY (BY
130 SIMILARITY)
131 FT DISULFID 1 12 BY SIMILARITY.
132 FT DISULFID 2 15 BY SIMILARITY.
133 FT DISULFID 8 17 BY SIMILARITY.
134 SQ SEQUENCE 17 AA; 1870 MW; E40021E0E96B9D82 CRC64;
135
136 Query Match 19.5%; Score 24; DB 1; Length 17;
137 Best Local Similarity 42.9%; Pred. No. 9.7e+02;
138 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
139
140 QY 1 FNRWCCL 7
141 : |||
142 : |||

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4 YGWTCWL 10

ILT 24
 ACTLG STANDARD; PRT; 19 AA.
 P56650;
 15-JUL-1999 (Rel. 38, Created)
 28-FEB-2003 (Rel. 41, Last sequence update)
 10-OCT-2003 (Rel. 42, Last annotation update)
 Lanthibiotic actagardine (Gardimycin).
 Actinoplanes liguriae.
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Micromonosporineae; Micromonosporaceae; Actinoplanes.
 NCBI_TaxID=69484;
 [1]
 PRELIMINARY SEQUENCE, AND STRUCTURE BY NMR.
 MEDLINE=91008698; PubMed=2211371;
 Kettnering J.K., Malabarba A., Vekey K., Cavallieri B.;
 "Sequence determination of actagardine, a novel lantibiotic, by
 homonuclear 2D NMR spectroscopy";
 J. Antibiot. 43:1082-1088(1990).
 [2]
 SEQUENCE, AND STRUCTURE BY NMR.
 MEDLINE=9525286; PubMed=7737178;
 Zimmermann N., Metzger J.W., Jung G.;
 "The tetracyclic lantibiotic actagardine. 1H-NMR and 13C-NMR
 assignments and revised primary structure.";
 Eur. J. Biochem. 228:786-797(1995).
 [3]
 STRUCTURE BY NMR.
 MEDLINE=97363218; PubMed=9219543;
 Zimmermann N., Jung G.;
 "The three-dimensional solution structure of the lantibiotic murein-
 biosynthesis-inhibitor actagardine determined by NMR.";
 Eur. J. Biochem. 246:809-819(1997).
 -1- FUNCTION: Has antibacterial activity against some Gram-positive
 bacteria. Has good antistreptococcal activity.
 -1- PTM: Maturation of lantibiotics involves the enzymic conversion of
 Thr, and Ser into dehydrated AA and the formation of thioether
 bonds with cysteines. The 14-19 beta-methylanthionine thioether
 bond is oxidized to a sulfoxide. This is followed by membrane
 translocation and cleavage of the modified precursor.
 -1- SIMILARITY: Belongs to the type B lantibiotic family.
 PIR; A58700; A58700.
 PDB; 1A11; 15-OCT-97.
 Antibiotic; Bacteriocin; Lantibiotic; Oxidation; Thioether bond;
 3D-STRUCTURE. 1 6 Lanthionine (Ser-Cys).
 CROSSLINK 7 12 Beta-methylanthionine (Thr-Cys).
 CROSSLINK 9 17 Beta-methylanthionine (Thr-Cys).
 CROSSLINK 14 19 Beta-methylanthionine sulfoxide
 (Thr-Cys).
 SEQUENCE 19 AA; 1946 MW; 5C138C7CEE8765B3 CRC64;

Query Match 19.5%; Score 24; DB 1; Length 19;
 Best Local Similarity 44.4%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

3 WRCLIPAC 11

4 WVTLTIEC 12

ILT 25
 PETMA STANDARD; PRT; 19 AA.
 Q10956;
 01-OCT-1996 (Rel. 34, Created)
 01-OCT-1996 (Rel. 34, Last sequence update)
 15-MAR-2004 (Rel. 43, Last annotation update)
 Corticostatin-related protein LCRP.
 Petromyzon marinus (Sea lamprey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 OC Petromyzontiformes; Petromyzontidae; Petromyzon.
 OX NCBI_TaxID=7757;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin;
 RX MEDLINE=96321324; PubMed=8759287;
 RA Conlon J.M., Sower S.A.;
 RT "Isolation of a peptide structurally related to mammalian
 corticostatin from the lamprey Petromyzon marinus.";
 RL Comp. Biochem. Physiol. 114B:133-137(1996).
 CC -1- FUNCTION: May have microbicidal activities. May inhibit
 corticotropin (ACTH) stimulated steroidogenesis and the microbial
 actions of the corticosteroids.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MASS SPECTROMETRY: MW=2201; MW ERR=0.4; METHOD=Electrospray.
 CC -1- SIMILARITY: Belongs to the corticostatin/defensin family.
 KW Defensin; Antibiotic.
 FT DISULFID 1 18 BY SIMILARITY.
 FT DISULFID 3 9 BY SIMILARITY.
 FT DISULFID 8 17 BY SIMILARITY.
 SQ SEQUENCE 19 AA; 2209 MW; 8D9CEDC71A199AE5 CRC64;

Query Match 19.5%; Score 24; DB 1; Length 19;
 Best Local Similarity 75.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 RCCL 7
 DB 7 RCCV 10

RESULT 26

CONO_CONST STANDARD; PRT; 9 AA.
 AC P05487;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Arg-conopressin S.
 OS Conus striatus (Striated cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6493;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=89058932; PubMed=3680228;
 RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
 Gray W.R., Olivera B.M., Cruz L.J.;
 RT "Invertebrate vasopressin/oxytocin homologs. Characterization of
 peptides from Conus geographus and Conus straitus venoms.";
 RL J. Biol. Chem. 262:15821-15824(1987).
 RN [2]
 RP REVIEW.
 RX MEDLINE=89024586; PubMed=3052286;
 RA Gray W.R., Olivera B.M., Cruz L.J.;
 RT "Peptide toxins from venomous Conus snails.";
 RL Annu. Rev. Biochem. 57:665-700(1988).
 CC -1- FUNCTION: Targets vasopressin-oxytocin related receptors.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- SIMILARITY: Belongs to the vasopressin/oxytocin family.
 DR PIR; B28495; B28495.
 DR InterPro; IPR000981; Neurhyp_horm.
 DR Pfam; PF00220; hormone4; 1.
 DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Amidation.
 FT DISULFID 1 6
 FT MOD RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 1031 MW; 17EB176EB4540050 CRC64;

Query Match 18.7%; Score 23; DB 1; Length 9;

st Local Similarity 50.0%; Pred. No. 1.4e+05;
tches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

6 CLIPACRR 13
|:|
1 CLIRNCP 8

LT 27
CONVR
CXL3 CONVR STANDARD; PRT; 12 AA.
P58809;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Lambda-conotoxin CM-X.
Conus marmoreus (Marble cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=42752;
[1]

SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
TISSUE=Venom;
MEDLINE=20564325; PubMed=10988292;
Balaji R.A., Ontake A., Sato K., Gopalakrishnakone P., Kini R.M.,
Seow K.T., Bay B.-H.;
"Lambda-conotoxins, a new family of conotoxins with unique disulfide
pattern and protein folding. Isolation and characterization from the
venom of Conus marmoreus";
J. Biol. Chem. 275:39516-39522 (2000).
-!- FUNCTION: Inhibits the neuronal noradrenaline transporter.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom duct.
-!- MASS SPECTROMETRY: MW=1262.77; MW ERR=0.07; METHOD=Electrospray.
-!- SIMILARITY: Belongs to the chi/lambda-conotoxin family.
Neurotoxin; Toxin; Hydroxylation.
DISULFID 3 12
DISULFID 4 9
MOD_RES 11 11 HYDROXYLATION
SEQUENCE 12 AA; 1251 MW; 277AAE2422D5AC8 CRC64;
ery Match 18.7%; Score 23; DB 1; Length 12;
st Local Similarity 42.9%; Pred. No. 9.8e+02;
tches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

5 CCLIPAC 11
|:|
3 CCGVSFC 9

LT 28
ESTAC
LYC ESTAC STANDARD; PRT; 18 AA.
P82175;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Lysozyme (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase) (Fragment).
Estigmenae acraea (Salt marsh moth).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
Actiidae; Estigmenae.
NCBI_TaxID=56594;
[1]

SEQUENCE, AND ENZYME REGULATION.
TISSUE=Hemocyte;
MEDLINE=97448947; PubMed=9303271;
Wittwer D., Weise C., Goetz P., Wiesner A.;
"LPS (lipopolysaccharide)-activated immune responses in a hemocyte
cell line from Estigmenae acraea (Lepidoptera).";
Dev. Comp. Immunol. 21:323-336 (1997).
-!- FUNCTION: Lysozymes have primarily a bacteriolytic function; those

in tissues and body fluids are associated with the monocyte-
macrophage system and enhance the activity of immunosagents (by
similarity).
-!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages between N-
acetyl-D-glucosamine and N-acetylmuramic acid in peptidoglycan
heteropolymers of the prokaryotes cell walls.
-!- ENZYME REGULATION: By lipopolysaccharide (LPS).
-!- SIMILARITY: Belongs to family 22 of glycosyl hydrolases.
DR InterPro; IPR001916; Glyco_Hydro_22.
DR PROSITE; PS00128; LACTALBUMIN LYSOZYME; PARTIAL.
KW Hydrolase; Glycosidase; Bacteriolytic enzyme.
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2213 MW; B229D8F5ECD07F57 CRC64;
Query Match 18.7%; Score 23; DB 1; Length 18;
Best Local Similarity 38.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 FNRCCCLIPACRR 13
|:|
Db 3 PATRCDDJVLRLK 15

RESULT 29
GON2_CHEPR
ID_GON2_CHEPR STANDARD; PRT; 10 AA.
AC P80678;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin II (Gonadotropin-releasing hormone II) (GnRH-II)
(Luliberin II).
OS Chelyosoma productum.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Corellidae; Chelyosoma.
OX NCBI_TaxID=71177;
RN [1]
RP SEQUENCE.
RA MEDLINE=96413669; PubMed=8816823;
RA Powell J.F.F., Reska-Skinner S.M., Prakash M.O., Fischer W.H.,
RA Park M., Rivier J.E., Craig A.G., Mackie G.O., Sherwood N.M.;
RT "Two new forms of gonadotropin-releasing hormone in a protochordate
and the evolutionary implications.";
RT Proc. Natl. Acad. Sci. U.S.A. 93:10461-10464 (1996).
RL -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
the secretion of both luteinizing and follicle-stimulating
hormones.
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: GnRH NEURONS LIE WITHIN BLOOD SINUSES CLOSE TO
THE GONADUCTS AND GONADS IN BOTH JUVENILES AND ADULTS, IMPLYING
THAT THE NEUROPEPTIDE IS RELEASED INTO THE BLOODSTREAM.
CC -!- MASS SPECTROMETRY: MW=1117.52; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the GnRH family.
DR InterPro; IPR02012; GnRH.
DR PROSITE; PS00473; GnRH.1.
KW Hormone; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 6 6 INTERCHAIN.
FT MOD_RES 10 10 AMIDATION (BY SIMILARITY).
SQ SEQUENCE 10 AA; 1135 MW; 284B38D1EEB735A3 CRC64;
Query Match 17.9%; Score 22; DB 1; Length 10;
Best Local Similarity 37.5%; Pred. No. 1.2e+03;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 NWRCCCLIP 9
|:|
Db 2 HWSLCHAP 9

RESULT 30
TINI_HOPTI

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TINI HOPTI STANDARD; PRT; 11 AA.
P82651:
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Tigerin-1.
Hoplomatrachus tigrinus (Indian bull frog) (Rana tigerina).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae;
Hoplomatrachus.
NCBI_TaxID=103373;
[1]
SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
TISSUE=Skin secretion;
PubMed11031261;
Purna Sai K., Nagaraj R., Sitaram N.;
Devi A.S., Nagaraj R., Vairamani M., Raju N.P.;
"Tigerinins: novel antimicrobial peptides from the Indian frog Rana
tigerina.";
J. Biol. Chem. 276:2701-2707(2001).
-!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,
S.aureus, M.luteus, P.putida and S.cerevisiae.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Skin.
-!- MASS SPECTROMETRY: MW=1342; METHOD=MALDI.
Amphibian defense peptide; Antibiotic; Fungicide; Amidation.
DISULFID 2 10
MOD RES 11 11
SEQUENCE 11 AA; 1344 MW; A2087DC960476056 CRC64;
Query Match 17.9%; Score 22; DB 1; Length 11;
st Local Similarity 50.0%; Pred. No. 1.3e+03;
tches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

5 CCLIPACR 12
|:|:|
2 CTMIPR 9

LT 31
-CAVPO STANDARD; PRT; 15 AA.
P83508;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Major allergen Cav p 2 (Fragment).
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
NCBI_TaxID=10141;
[1]
SEQUENCE
TISSUE=Hair;
MEDLINE=22707217; PubMed=12823123;
Fahlbusch B., Rudeschko O., Schlott B., Henzgen M., Schlenvoigt G.,
Schubert H., Kinne R.W.;
"Further characterization of IGS-binding antigens from guinea pig
hair as new members of the lipocalin family.";
Allergy 58:629-634(2003).
-!- SUBCELLULAR LOCATION: Secreted.
-!- ALLERGEN: Causes an allergic reaction in human. Binds to IgE. Is a
cause of guinea pig hair allergy.
-!- SIMILARITY: Belongs to the lipocalin family.
GO; GO:0016068; P:immediate hypersensitivity response; NAS.
InterPro; IPR000566; Lipocln_cytFAP.
PROSITE; PS00213; LIPOCALIN_PARTIAL.
Lipocalin; Allergen. 15
NON_TER 15
SEQUENCE 15 AA; 1751 MW; DGA053A7A23EC26 CRC64;
Query Match 17.9%; Score 22; DB 1; Length 15;
st Local Similarity 100.0%; Pred. No. 1.7e+03;

TINI HOPTI STANDARD; PRT; 11 AA.
P82651:
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Tigerin-1.
Hoplomatrachus tigrinus (Indian bull frog) (Rana tigerina).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae;
Hoplomatrachus.
NCBI_TaxID=103373;
[1]
SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
TISSUE=Skin secretion;
PubMed11031261;
Purna Sai K., Nagaraj R., Sitaram N.;
Devi A.S., Nagaraj R., Vairamani M., Raju N.P.;
"Tigerinins: novel antimicrobial peptides from the Indian frog Rana
tigerina.";
J. Biol. Chem. 276:2701-2707(2001).
-!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,
S.aureus, M.luteus, P.putida and S.cerevisiae.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Skin.
-!- MASS SPECTROMETRY: MW=1342; METHOD=MALDI.
Amphibian defense peptide; Antibiotic; Fungicide; Amidation.
DISULFID 2 10
MOD RES 11 11
SEQUENCE 11 AA; 1344 MW; A2087DC960476056 CRC64;
Query Match 17.9%; Score 22; DB 1; Length 11;
st Local Similarity 50.0%; Pred. No. 1.3e+03;
tches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

5 CCLIPACR 12
|:|:|
2 CTMIPR 9

LT 31
-CAVPO STANDARD; PRT; 15 AA.
P83508;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Major allergen Cav p 2 (Fragment).
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
NCBI_TaxID=10141;
[1]
SEQUENCE
TISSUE=Hair;
MEDLINE=22707217; PubMed=12823123;
Fahlbusch B., Rudeschko O., Schlott B., Henzgen M., Schlenvoigt G.,
Schubert H., Kinne R.W.;
"Further characterization of IGS-binding antigens from guinea pig
hair as new members of the lipocalin family.";
Allergy 58:629-634(2003).
-!- SUBCELLULAR LOCATION: Secreted.
-!- ALLERGEN: Causes an allergic reaction in human. Binds to IgE. Is a
cause of guinea pig hair allergy.
-!- SIMILARITY: Belongs to the lipocalin family.
GO; GO:0016068; P:immediate hypersensitivity response; NAS.
InterPro; IPR000566; Lipocln_cytFAP.
PROSITE; PS00213; LIPOCALIN_PARTIAL.
Lipocalin; Allergen. 15
NON_TER 15
SEQUENCE 15 AA; 1751 MW; DGA053A7A23EC26 CRC64;
Query Match 17.9%; Score 22; DB 1; Length 15;
st Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 NWR 4
DB 11 NWR 13

RESULT 32
UC08_MAIZE STANDARD; PRT; 15 AA.
ID UC08_MAIZE STANDARD; PRT; 15 AA.
AC P80614;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 159)
(Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Ricciardi F., Morin C., Damerval C., Huet J.-C.,
Pernollet J.-C., Zivy M., de Vienne D.;
"The maize two dimensional gel protein database: towards an integrated
genome analysis program.";
RT Theor. Appl. Genet. 93:997-1005(1996).
RL CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
protein is: 6.4, its MW is: 38.8 kDa.
CC -!- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
family.
CC Maize-2DPAGE; P80614; COLEOPTILE.
DR MaizeDB; 123934; -.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1785 MW; 1978B1D6AB4DDF8D CRC64;
Query Match 17.9%; Score 22; DB 1; Length 15;
Best Local Similarity 37.5%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 2 NWRCLIP 9
DB 2 DWRNAMP 9

RESULT 33
OXYT_BUFRE STANDARD; PRT; 9 AA.
ID OXYT_BUFRE STANDARD; PRT; 9 AA.
AC P42955;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Seritocin ([Sers, Iles]-oxytocin).
OS Bufo regularis (leopard toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Bufonidae; Bufo.
OX NCBI_TaxID=8390;
RN [1]
RP SEQUENCE
TISSUE=Hypothalamic neurointermediate lobe;
RC MEDLINE=96059313; PubMed=7591488;
RA Chauvet J., Michel G., Ouedraogo Y., Chou J., Chait B.T., Acher R.;
"A new neurohypophyseal peptide, seritocin ([Sers, Iles]-oxytocin),
identified in a dryness-resistant African toad, Bufo regularis.";
Int. J. Pept. Protein Res. 45:482-487(1995).
RL CC -!- FUNCTION: Devoid of oxytocic activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR InterPro; IPR000981; Neurohyp_horm.
DR Pfam; PF00220; hormone4; 1.

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PROSITE; PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
Hormone; Amidation.
DISULFID 1 6
MOD_RES 9 9 AMIDATION.
SEQUENCE 9 AA; 983 MW; 17FF476EAS6D04B CRC64;

very Match 17.1%; Score 21; DB 1; Length 9;
est Local Similarity 50.0%; Pred. No. 1.4e+05;
atches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

6 CLIPAC 11
| | | |
1 CYIQSC 6

JLT 34
I_CYPCA STANDARD; PRT; 9 AA.
P23879;
01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Vasotocin.
Cyprinus carpio (Common carp), and
Petrionyzon marinus (Sea lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Cyprinus.
NCBI_TaxID=7962, 7757;
[1]
SEQUENCE.
SPECIES=C.carpio; TISSUE=Pituitary;
Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
"Characterization of neurohypophyseal hormones from a fresh water bony
fish, the carp (Cyprinus carpio). Comparison with hormones from sea
water bony fishes.";
Comp. Biochem. Physiol. 14:245-254 (1965).
[2]
SEQUENCE.
SPECIES=P.marinus; TISSUE=Pituitary;
MEDLINE=88225976; PubMed=3371648;
Lane T.F., Sower S.A., Kawauchi H.;
"Arginine vasotocin from the pituitary gland of the lamprey
(Petrionyzon marinus): isolation and amino acid sequence.";
Gen. Comp. Endocrinol. 70:152-157 (1988).
-1- FUNCTION: ANTIDIURETIC HORMONE
-1- SIMILARITY: Belongs to the vasopressin/oxytocin family.
PIR; B61364; B61364.
PIR; S06375; S06375.
InterPro; IPR000981; Neurohyp_horm.
Pfam; PF00220; hormones4; 1.
PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
Hormone; Amidation.
DISULFID 1 6
MOD_RES 9 9 AMIDATION.
SEQUENCE 9 AA; 1053 MW; 17EB176EB456D04B CRC64;

very Match 17.1%; Score 21; DB 1; Length 9;
est Local Similarity 50.0%; Pred. No. 1.4e+05;
atches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

6 CLIPACR 13
| | | |
1 CYIQNCP 8

JLT 35
A_CATCO STANDARD; PRT; 12 AA.
P04558;
13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)

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DE Urotensin IIA (U-IIA) (UIIA).
OS Catostomus commersoni (White sucker).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Catostomidae; Catostomus.
OX NCBI_TaxID=7971;
RN [1]
RP SEQUENCE.
RX MEDLINE=84041959; PubMed=6138758;
RA McMaster D., Lederis K.;
RT "Isolation and amino acid sequence of two urotensin II peptides from
RT Catostomus commersoni urophyses.";
RL Peptides 4:367-373 (1983).
CC -1- FUNCTION: Urotensin is found in the teleost caudal neurosecretory
CC system. It has a suggested role in osmoregulation and as a
CC corticotropin-releasing factor.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the urotensin 2 family.
DR FIR; JS0423; JS0423.
DR InterPro; IPR001483; Urotensin_II.
DR Pfam; PF02083; Urotensin_II; 1.
DR PROSITE; PS00984; UROTENSIN_II; 1.
KW Hormone.
FT DISULFID 6 11
SQ SEQUENCE 12 AA; 1336 MW; 969C76DBB879CEBA CRC64;

Query Match 17.1%; Score 21; DB 1; Length 12;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 WRCCCL 7
| | | |
Db 8 WKYCV 12

Search completed: February 18, 2004, 06:27:56
Job time : 13 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

protein - protein search, using sw model

on: February 18, 2004, 06:15:19 ; Search time 38 seconds
(without alignments)
157.759 Million cell updates/sec

le: US-09-806-376-1

fect score: 123

lence: 1 FNRWCLIPACRNHHKFC 19

ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ched: 1017041 seqs, 315518202 residues

al number of hits satisfying chosen parameters: 6498

imum DB seq length: 0

imum DB seq length: 19

t-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

abase :

1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query Match	Length	ID	Description
1	36	29.3	9	10 Q9FSZ2	Q9fsz2 cicer ariet
2	30	24.4	19	12 Q65340	Q65340 autographa
3	29	23.6	13	4 QJUM29	QJum29 homo sapien
4	29	23.6	17	4 Q16228	Q16228 homo sapien
5	28.5	23.2	17	6 Q9XSG1	Q9xsg1 bos taurus
6	28	22.8	10	8 Q9T2P3	Q9t2p3 rattus sp.
7	28	22.8	17	5 Q9I6R4	Q9i6r4 conus imper
8	27.5	22.4	17	2 Q9R581	Q9r581 vibrio chol
9	27.5	22.4	18	2 Q9R580	Q9r580 vibrio chol
10	27.5	22.4	19	2 Q9R579	Q9r579 vibrio chol
11	27	22.0	15	4 Q15344	Q15344 homo sapien
12	26	21.1	15	15 Q85713	Q85713 rous sarcom
13	26	21.1	19	11 Q8CJ05	Q8cj05 mesocricetu
14	25	20.3	14	4 Q9BXR7	Q9bxr7 homo sapien
15	25	20.3	15	2 Q7WRZ1	Q7wrz1 flavobacter
16	25	20.3	17	5 Q816R5	Q816r5 conus imper

17	25	20.3	19	15	Q905K4	Q905k4 human immun
18	24	19.5	8	11	Q80WD6	Q80wd6 mus musculus
19	24	19.5	8	11	Q80WD5	Q80wd5 mus musculus
20	24	19.5	11	11	Q97330	Q97330 mus musculus
21	24	19.5	11	12	Q89269	Q89269 xestia c-ni
22	24	19.5	11	13	Q9P822	Q9p822 xenopus lae
23	24	19.5	17	4	Q86V63	Q86v63 homo sapien
24	24	19.5	17	12	Q8B4C4	Q8b4c4 hepatitis b
25	24	19.5	18	8	Q78379	Q78379 theileria a
26	24	19.5	19	4	Q9UMW9	Q9umw9 homo sapien
27	24	19.5	19	8	Q9XMB5	Q9xmb5 aegilops ta
28	23	18.7	12	12	Q88577	Q88577 theiler's e
29	23	18.7	12	12	Q88578	Q88578 theiler's e
30	23	18.7	12	12	Q88579	Q88579 theiler's e
31	23	18.7	12	12	Q88575	Q88575 theiler's e
32	23	18.7	12	12	Q88580	Q88580 theiler's e
33	23	18.7	12	12	Q88582	Q88582 theiler's e
34	23	18.7	12	12	Q88581	Q88581 theiler's e
35	23	18.7	12	12	Q88576	Q88576 theiler's e
36	23	18.7	13	12	Q9ELV1	Q9elv1 hepatitis b
37	23	18.7	19	8	Q9ZIW7	Q9ziw7 aphidius ro
38	23	18.7	19	8	Q9ZYW5	Q9zyw5 jarra phoro
39	23	18.7	19	8	Q9ZY71	Q9zy71 heterospilu
40	23	18.7	19	11	Q925G8	Q925g8 mus musculus
41	23	18.7	19	15	Q90RG1	Q90rg1 human immun
42	22	17.9	8	6	Q02831	Q02831 oryctolagus
43	22	17.9	13	8	Q9T569	Q9t569 zea mays (m
44	22	17.9	13	11	Q60517	Q60517 mus musculus
45	22	17.9	14	2	P71199	P71199 escherichia
46	22	17.9	14	2	Q93C11	Q93c11 escherichia
47	22	17.9	14	11	Q81027	Q81027 mus musculus
48	22	17.9	16	12	Q9YQ11	Q9yq11 transmissib
49	22	17.9	16	13	Q9PTT5	Q9ptt5 gallus gall
50	22	17.9	17	2	Q841R6	Q841r6 yersinia pe

ALIGNMENTS

RESULT 1

Q9FSZ2	PRELIMINARY;	PRT;	9 AA.
ID	Q9FSZ2		
AC	Q9FSZ2;		
DT	01-MAR-2001 (TrEMBLrel. 16, Created)		
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Hypothetical protein (Fragment).		
OS	Cicer arietinum (Chickpea) (Garbanzo)		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;		
OC	eurosid1; Fabales; Fabaceae; Papilionoideae; Cicereae; Cicer.		
OX	NCBI_TaxID=3827;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=cv. Castellana; TISSUE=Etolated epicotyl;		
RA	Dopico B.; Jimenez T.; Labrador E.;		
RT	"cDNA clones expressed in etolated Cicer arietinum epicotyls.";		
RL	Submitted (SEP-2000) to the EMBL/GenBank/DDJB databases.		
DR	EMBL; AJ299069; CAC10216.1; -		
KW	Hypothetical protein.		
FT	NON TER		
SQ	SEQUENCE 9 AA; 990 MW; 9441BDDAA7272EBE CRC64;		

Query Match 29.3%; Score 36; DB 10; Length 9;
Best Local Similarity 71.4%; Pred. No. 1e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCLIPAC 11
DB 2 CCLLDAC 8

RESULT 2

340 Q65340 PRELIMINARY; PRT; 19 AA.
 Q65340;
 01-NOV-1996 (TrEMBLrel. 01, Created)
 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DNA polymerase (Fragment).
 Autographa californica nuclear polyhedrosis virus (AcMNPV).
 Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 Nucleopolyhedrovirus.
 NCBI_TaxID=46015;
 [1]
 SEQUENCE FROM N.A.
 STRAIN=L1;
 MEDLINE=89073763; PubMed=3059678;
 Tonalski M.D., Wu J., Miller L.K.;
 "The location, sequence, transcription, and regulation of a
 baculovirus DNA polymerase gene.";
 Virology 167:591-600(1988).
 [2]
 SEQUENCE FROM N.A.
 STRAIN=L1;
 MEDLINE=89381697; PubMed=2674327;
 Wu J., Miller L.K.;
 "Sequence, transcription and translation of a late gene of the
 Autographa californica nuclear polyhedrosis virus encoding a 34.8K
 polypeptide.";
 J. Gen. Virol. 70:2449-2459(1989).
 EMBL; D00583; BAA00460.1; --
 NON TER 1
 SEQUENCE 19 AA; 2314 MW; C9DD06D721F17972 CRC64;
 Query Match 24.4%; Score 30; DB 12; Length 19;
 Best Local Similarity 55.6%; Pred. No. 7.1e+02;
 atches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 11 CRRNHKFC 19
 |||||
 5 CANTYKFC 13
 |||||
 ULT 3
 ME9
 Q9UME9 PRELIMINARY; PRT; 13 AA.
 Q9UME9
 01-MAY-2000 (TrEMBLrel. 13, Created)
 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 Elastin (Fragment).
 ELN.
 Homo sapiens (Human).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=87274906; PubMed=3038460;
 Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J.,
 Rosenbloom J., Ornstein-Goldstein N.;
 "Structure of the 3' region of the human elastin gene: great abundance
 of Alu repetitive sequences and few coding sequences.";
 Connect. Tissue Res. 16:197-211(1987).
 [2]
 SEQUENCE FROM N.A.
 MEDLINE=93091639; PubMed=9873040;
 Zhang M.C., He L., Giro M., Yong S.L., Tiller G.B., Davidson J.M.;
 "Curis laxa arising from frameshift mutations in exon 30 of the
 elastin gene (ELN).";
 J. Biol. Chem. 274:981-986(1999).
 EMBL; U77846; AAC9789.1; --
 NON TER 1
 SEQUENCE 13 AA; 1348 MW; 43E12DFB5AE5BDD3 CRC64;

Query Match 23.6%; Score 29; DB 4; Length 13;
 Best Local Similarity 54.5%; Pred. No. 7.3e+02;
 Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 6 CLIPACRRNHK 16
 |||||
 Db 3 CLGKACGRK 13
 |||||
 RESULT 4
 Q16228 PRELIMINARY; PRT; 17 AA.
 ID Q16228;
 AC Q16228;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE Peripherin (Fragment).
 GN RDS.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94290510; PubMed=8019570;
 RA Gruning G., Millan J.M., Meins M., Benevto M., Caballero M.,
 RA Apfelstedt-Sylla E., Bosch R., Zrenner E., Prieto F., Gal A.;
 RT "Mutations in the human peripherin/RDS gene associated with autosomal
 dominant retinitis pigmentosa.";
 Hum. Mutat. 3:321-323(1994).
 RL EMBL; S73627; AAB31191.1; --
 DR NON TER 1
 FT NON TER 1
 SQ SEQUENCE 17 AA; 2342 MW; 96828BA695A9D1EB CRC64;
 Query Match 23.6%; Score 29; DB 4; Length 17;
 Best Local Similarity 38.9%; Pred. No. 9.3e+02;
 Matches 7; Conservative 2; Mismatches 5; Indels 4; Gaps 1;
 QY 1 FNRWCLIPACRRNHKFF 18
 :|||:|:
 Db 1 WRWR----RACRRPGRPF 14
 :|||:|:
 RESULT 5
 Q9XSG1 PRELIMINARY; PRT; 17 AA.
 ID Q9XSG1
 AC Q9XSG1
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE SMCX (Fragment).
 GN SMCX.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Poloumienko A., Blecher S.;
 RT "Exon-intron structure of SMCX and SMCY genes in bovine and swine.";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DDJ databases.
 DR EMBL; AF135448; AAD34440.1; --
 FT NON TER 1
 FT NON TER 17
 SQ SEQUENCE 17 AA; 1927 MW; 10351B0D516D16F0 CRC64;
 Query Match 23.2%; Score 28.5; DB 6; Length 17;
 Best Local Similarity 55.6%; Pred. No. 1.1e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 3; Gaps 1;
 QY 3 WRCLIPAC 11

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|||||
9 WRC---PKC 14

JLT 6
JFP3
Q9T2P3 PRELIMINARY; PRT; 10 AA.
Q9T2P3;
01-MAY-2000 (TREMELrel. 13, Created)
01-MAY-2000 (TREMELrel. 13, Last sequence update)
01-JUN-2002 (TREMELrel. 21, Last annotation update)
Cytochrome P-450 27/25-HYDROXYLASE=52 kDa isoform (Fragment).
Rattus sp.
Mitochondrion.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10118;
[1]
SEQUENCE.
MEDLINE=91355184; PubMed=1883820;
Addya S., Zheng Y.M., Shayig R.M., Fan J.Y., Avadhani N.G.;
"Characterization of a female-specific hepatic mitochondrial
cytochrome P-450 whose steady-state level is modulated by
testosterone.";
Biochemistry 30:8323-8330(1991).
NON_TER 1
NON_TER 10
SEQUENCE 10 AA; 1092 MW; 316CFEFA072DDC7 CRC64;

Query Match 22.8%; Score 28; DB 8; Length 10;
Best Local Similarity 55.6%; Pred. No. 8.5e+02;
Matches 5; Conservative 2; Mismatches 0; Gaps 0;
Indels 0;

8 IPACRRNHK 16
|||||
2 IPALRDHE 10

JLT 7
SR4
Q816R4 PRELIMINARY; PRT; 17 AA.
Q816R4;
01-MAR-2003 (TREMELrel. 23, Created)
01-MAR-2003 (TREMELrel. 23, Last sequence update)
01-MAR-2003 (TREMELrel. 23, Last annotation update)
Alpha-conotoxin ImI precursor (Fragment).
Conus imperialis (Imperial cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hyposogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=35631;
[1]
SEQUENCE FROM N.A.
PubMed=12384509;
Ellison M.A., McIntosh J.M., Olivera B.M.;
"alpha-Conotoxins ImI and ImII: similar alpha 7 nicotinic receptor
antagonists act at different sites.";
J. Biol. Chem. 278:757-764(2003).
EMBL; AY159318; AA78128.1; -.
NON_TER 1
NON_TER 5
CHAIN 17 AA; 1938 MW; 9590D9CEA50279CF CRC64;
SEQUENCE 17 AA; 1938 MW; 9590D9CEA50279CF CRC64;

Query Match 22.8%; Score 28; DB 5; Length 17;
Best Local Similarity 57.1%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

5 CCLIPAC 11
|||||
6 CCSDPRC 12
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JLT 8

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Q9R581
ID Q9R581 PRELIMINARY; PRT; 17 AA.
AC Q9R581;
01-MAY-2000 (TREMELrel. 13, Created)
01-MAY-2000 (TREMELrel. 13, Last sequence update)
01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE 01-ST-1, NAG-ST, VM-ST-HEAT-stable enterotoxin.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
SEQUENCE.
MEDLINE=93314823; PubMed=8325391;
Yoshino K., Miyachi M., Takao T., Bag P.K., Huang X., Nair G.B.,
Takeda T., Shimonishi Y.;
"Purification and sequence determination of heat-stable enterotoxin
elaborated by a cholera toxin-producing strain of Vibrio cholerae
O1.";
FEBS Lett. 326:83-86(1993).
DR HSSP; P01559; 1ETN.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; P:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001489; Enterotoxin_HS.
DR Pfam; PF02048; Enterotoxin_HS_1.
DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
DR SEQUENCE 17 AA; 1821 MW; 30FF036D018D601C CRC64;

Query Match 22.4%; Score 27.5; DB 2; Length 17;
Best Local Similarity 60.0%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 5 CCLI---PAC 11
DB 3 CCEICNPAC 12

RESULT 9
Q9R580
ID Q9R580 PRELIMINARY; PRT; 18 AA.
AC Q9R580;
01-MAY-2000 (TREMELrel. 13, Created)
01-MAY-2000 (TREMELrel. 13, Last sequence update)
01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE 01-ST-2, VC-H-ST-HEAT-stable enterotoxin.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
SEQUENCE.
MEDLINE=93314823; PubMed=8325391;
Yoshino K., Miyachi M., Takao T., Bag P.K., Huang X., Nair G.B.,
Takeda T., Shimonishi Y.;
"Purification and sequence determination of heat-stable enterotoxin
elaborated by a cholera toxin-producing strain of Vibrio cholerae
O1.";
FEBS Lett. 326:83-86(1993).
DR HSSP; P01559; 1ETN.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; P:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001489; Enterotoxin_HS.
DR Pfam; PF02048; Enterotoxin_HS_1.
DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
DR SEQUENCE 18 AA; 1934 MW; 3080692D018D601C CRC64;

Query Match 22.4%; Score 27.5; DB 2; Length 18;
Best Local Similarity 60.0%; Pred. No. 1.7e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 5 CCLI---PAC 11
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|||||
4 CCEICNPAC 13

ULT 10

579 Q9R579 PRELIMINARY; PRT; 19 AA.
Q9R579; 01-MAY-2000 (TREMBlrel. 13, Created)
01-MAY-2000 (TREMBlrel. 13, Last sequence update)
01-JUN-2003 (TREMBlrel. 24, Last annotation update)
01-ST-3=H9AT-stable enterotoxin.
Vibrio cholerae.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
NCBI_TaxID=666;
[1]
SEQUENCE
MEDLINE=93314823; PubMed=8325391;
Yoshino K., Miyachi M., Takao T., Bag P.K., Huang X., Nair G.B.,
Takeda T., Shimonishi Y.;
"Purification and sequence determination of heat-stable enterotoxin
elaborated by a cholera toxin-producing strain of Vibrio cholerae
O1";
FEBS Lett. 326:83-86(1993).
HSP; P01559; IETN.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0015070; F:toxin activity; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro: IPR001489; Enterotoxin.HS.
Pfam: PF02048; Enterotoxin.HS.1
PROSITE: PS00273; ENTEROTOXIN_H STABLE; 1.
SEQUENCE 19 AA; 2048 MW; 308015F1A18D601C CRC64;

Query Match 22.4%; Score 27.5; DB 2; Length 19;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

5 CCLI---PAC 11
|||||
5 CCEICNPAC 14

Q15344 PRELIMINARY; PRT; 15 AA.
Q15344; 01-NOV-1996 (TREMBlrel. 01, Created)
01-NOV-1999 (TREMBlrel. 12, Last sequence update)
01-NOV-1999 (TREMBlrel. 12, Last annotation update)
Aml1 protein (Fragment).
AML1.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.

MEDLINE=96226397; PubMed=8631417;
Levanon D., Bernstein Y., Negreanu V., Ghazi M.C., Bar-Am I.,
Aloya R., Goldenberg D., Lotem J., Groner Y.;
"A large variety of alternatively spliced and differentially expressed
mRNAs are encoded by the human acute myeloid leukemia gene AML1";
DNA Cell Biol. 15:175-185(1996).
EMBL; X90980; CAA62467.2;
NON_TER 1
NON_TER 15 15
SEQUENCE 15 AA; 1931 MW; 228A48BEE675423 CRC64;

Query Match 22.0%; Score 27; DB 4; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 PACRR 13
|:|:|
DB 9 PSRR 13

RESULT 12

Q85713 PRELIMINARY; PRT; 15 AA.
AC Q85713;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE 29 (RSV-29) src (Fragment).
OS Rous sarcoma virus.
OC Viruses; Retroviral viruses; Retroviridae; Alpharetrovirus.
OX NCBI_TaxID=11886;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85265036; PubMed=2991593;
Dutta A., Wang L.-H., Hanafusa T., Hanafusa H.;
"Partial nucleotide sequence of Rous sarcoma virus-29 provides
evidence that the original rous sarcoma virus was replication
defective";
J. Virol. 55:728-735(1985).
DR EMBL; M1117; AAA42556.1;
FT NON_TER 1
SQ SEQUENCE 15 AA; 1597 MW; DB53E0F31273C5C1 CRC64;
Query Match 21.1%; Score 26; DB 15; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.5e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLPAC 11
|:|:|
DB 5 LLPAC 9

RESULT 13

Q8CJ05 PRELIMINARY; PRT; 19 AA.
AC Q8CJ05;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Cyclic D1 (Fragment).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RA Hilton T.L., Dunphy E.L., Wang E.H.;
"TAF1 (TAFII250) Histone Acetyltransferase Activity in Activation of
the Cyclin D1 Proximal Promoter";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF539477; AAN59789.1;
FT NON_TER 19
SQ SEQUENCE 19 AA; 2307 MW; 83E3341F29C52279 CRC64;

Query Match 21.1%; Score 26; DB 11; Length 19;
Best Local Similarity 44.4%; Pred. No. 3.1e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 CCLIPACRR 13
|:|:|
DB 7 CCEVETIRR 15

RESULT 14

Q9BXR7 PRELIMINARY; PRT; 14 AA.
ID Q9BXR7
AC Q9BXR7;

01-JUN-2001 (TrEMBLrel. 17, Created)
 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 Interleukin 10 (Fragment)
 Homo sapiens (Human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=21136366; PubMed=11238636;
 Gibson A.W., Edberg J.C., Wu J., Westendorp R.G.J., Huizinga T.W.J.,
 Kimberly R.P.,
 "Novel Single Nucleotide Polymorphisms in the Distal IL-10 Promoter
 Affect IL-10 Production and Enhance the Risk of Systemic Lupus
 Erythematosus."
 J. Immunol. 166:3915-3922(2001).
 EMBL; AF295024; AAK19173.1;
 NON TER 14
 SEQUENCE 14 AA; 1504 MW; 438B64AB431997B7 CRC64;
 Query Match 20.3%; Score 25; DB 4; Length 14;
 Best Local Similarity 75.0%; Pred. No. 3.4e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

5 CCLJ 8
 8 CCLV 11

JUL 15
 RZ1
 QWRZ1 PRELIMINARY; PRT; 15 AA.
 01-OCT-2003 (TrEMBLrel. 25, Created)
 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 Hypothetical protein.
 Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales;
 Flavobacteriaceae; Flavobacterium.
 NCBI_TaxID=96345;
 [1]
 SEQUENCE FROM N.A.
 STRAIN=FFC817, Ch. 8-80, TG-P01/88, OK99801, OKW9801, YMY9520, YNU9803,
 FPC945, FPC840, FPC924, FPC956, OK99805, and YNA9801;
 Izumi S., Aranishi F., Wakabayashi H.,
 "Genotyping of Flavobacterium psychrophilum using PCR-RFLP analysis."
 Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 EMBL; AB097201; BAC76960.1;
 EMBL; AB097202; BAC76961.1;
 EMBL; AB097203; BAC76962.1;
 EMBL; AB097204; BAC76963.1;
 EMBL; AB097205; BAC76964.1;
 EMBL; AB097206; BAC76965.1;
 EMBL; AB097207; BAC76966.1;
 EMBL; AB097208; BAC76967.1;
 EMBL; AB097209; BAC76968.1;
 EMBL; AB097210; BAC76969.1;
 EMBL; AB097211; BAC76970.1;
 EMBL; AB097212; BAC76971.1;
 EMBL; AB097213; BAC76972.1;
 Hypothetical protein.
 SEQUENCE 15 AA; 1903 MW; 668EE50085B3F71D CRC64;

Query Match 20.3%; Score 25; DB 2; Length 15;
 Best Local Similarity 42.9%; Pred. No. 3.6e+03;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

12 RNRHKKF 18
 : : : : :
 9 KQNHAKY 15

RESULT 16
 Q816R5 PRELIMINARY; PRT; 17 AA.
 ID Q816R5
 AC Q816R5
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Alpha-conotoxin ImI precursor (Fragment).
 OS Conus imperialis (Imperial cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbecconcha; Hypogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 NCBI_TaxID=35631;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=12384509;
 RA Ellison M.A., McIntosh J.M., Olivera B.M.,
 RT "alpha-Conotoxins ImI and ImII: similar alpha 7 nicotinic receptor
 antagonists act at different sites."
 RL J. Biol. Chem. 278:757-764(2003).
 DR EMBL; AY159317; AAN78127.1;
 FT NON TER 1
 FT CHAIN 5 17 ALPHA-CONOTOXIN IMI.
 SQ SEQUENCE 17 AA; 2096 MW; CF90D9CEBB4C79CC CRC64;

Query Match 20.3%; Score 25; DB 5; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WRC 5
 DB 14 WRC 16

RESULT 17
 Q905K4 PRELIMINARY; PRT; 19 AA.
 ID Q905K4
 AC Q905K4
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Tat protein (Fragment).
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=96CG16;
 RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,
 RA N'Doundou-N'Kodia M.-Y., M'Pandi M., Harada Y., Hayami M.,
 RA Ichimura H., Parra H.-J.,
 RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
 RT Republic of Congo-Brazzaville."
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF410438; AAL10218.1;
 FT NON TER 1
 FT NON TER 19
 SQ SEQUENCE 19 AA; 2224 MW; B479FE3CB9E68238 CRC64;

Query Match 20.3%; Score 25; DB 15; Length 19;
 Best Local Similarity 40.0%; Pred. No. 4.4e+03;
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 9 PACRRNHKKF 18
 DB 7 PNSNQHQDF 16

RESULT 18
 Q80WD6 PRELIMINARY; PRT; 8 AA.
 ID Q80WD6
 AC Q80WD6;

01-JUN-2003 (TReMBLrel. 24, Created)
 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 Olfactory receptor (Fragment).
 GENE 154
 Mus musculus (Mouse).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=94373818; PubMed=8087849;
 Chess A., Simon I., Cedar H., Axel R.;
 "Allelic inactivation regulates olfactory receptor gene expression.";
 Cell 78:823-834(1994).
 EMBL; S73844; AAP21081.1; -.
 GO; GO:0004872; F:receptor activity; IEA.
 Receptor.
 NON TER
 SEQUENCE 8 AA; 1000 MW; F161A1E454140B16 CRC64;
 Query Match 19.5%; Score 24; DB 11; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 [1]
 12 RRNH 15
 |||||
 3 RRNH 6
 RESULT 19
 ID P89269 PRELIMINARY; PRT; 8 AA.
 AC P89269;
 DT 01-JUN-2003 (TReMBLrel. 24, Created)
 DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 Olfactory receptor (Fragment).
 GENE 154.
 Mus spretus (Western wild mouse).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10096;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=94373818; PubMed=8087849;
 Chess A., Simon I., Cedar H., Axel R.;
 "Allelic inactivation regulates olfactory receptor gene expression.";
 Cell 78:823-834(1994).
 EMBL; S73845; AAP21082.1; -.
 GO; GO:0004872; F:receptor activity; IEA.
 Receptor.
 NON TER
 SEQUENCE 8 AA; 986 MW; F165B1E454140B16 CRC64;
 Query Match 19.5%; Score 24; DB 11; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 [1]
 12 RRNH 15
 |||||
 3 RRNH 6
 RESULT 20
 ID P97330 PRELIMINARY; PRT; 11 AA.
 AC P97330;
 DT 01-MAY-1997 (TReMBLrel. 03, Created)
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 CD45-AP (LSM-1).
 PTPRCAP.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97124850; PubMed=8954783;
 RA Bruyns E., Mincheva A., Bruyns R.M., Kirchgessner H., Weitz S.,
 RA Lichter P., Meyer S., Schraven B.;
 RT "Sequence, genomic organization and chromosomal localization of the
 human LPRP (PTPRCAP) and Mouse CD45-AP/LSM-1 genes.";
 RL Genomics 38:79-83(1996).
 DR EMBL; X97268; CAA65923.1; -.
 DR MGD; MGI:97811; Ptprcap.
 SQ SEQUENCE 11 AA; 1150 MW; 50695413B5A772C7 CRC64;
 Query Match 19.5%; Score 24; DB 11; Length 11;
 Best Local Similarity 60.0%; Pred. No. 4e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 6 CLIPA 10
 |||||
 Db 3 CLVPS 7
 RESULT 21
 ID P89269 PRELIMINARY; PRT; 11 AA.
 AC P89269;
 DT 01-MAY-1997 (TReMBLrel. 03, Created)
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE DNA binding protein homolog (Fragment).
 OS Xestia c-nigrum granulosis virus (XngV) (Xestia c-nigrum
 OS granulovirus).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
 OX NCBI_TaxID=51677;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SFRAIN-alpha-4;
 RX MEDLINE=98271593; PubMed=9608666;
 RA Goto C., Hayakawa T., Maeda S.;
 RT "Genome organization of Xestia c-nigrum granulovirus.";
 RL Virus Genes 16:199-210(1998).
 DR EMBL; U70897; AAB46487.1; -.
 FT NON TER 1
 SQ SEQUENCE 11 AA; 1371 MW; 6F05444F52C1E454 CRC64;
 Query Match 19.5%; Score 24; DB 12; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 RRNH 15
 |||||
 Db 3 RRNH 6
 RESULT 22
 ID O9PS22 PRELIMINARY; PRT; 11 AA.
 AC O9PS22;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Hydrin 1', VASOTOCINYL-GLY-LYS.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93200145; PubMed=8452872;

Iwamuro S., Hayashi H., Kikuyama S.;
 "An additional arginine-vasotocin-related peptide, vasotocinyl-Gly-Lys, in Xenopus neurohypophysis";
 Biochim. Biophys. Acta 1176:143-147(1993).
 GO: GO:0005576; C:extracellular; IEA.
 GO: GO:0005185; F:neurohypophyseal hormone activity; IEA.
 InterPro: IPR000981; Neurohyp_horm.
 Pfam: PF00220; hoxmone4; 1.
 PROSITE: PS00264; NEUROHYPOPHYS HORM; 1.
 SEQUENCE 11 AA; 1238 MW; C05B57EB176EB456 CRC64;

Query Match 19.5%; Score 24; DB 13; Length 11;
 Best Local Similarity 45.5%; Pred. No. 4e+03;
 Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

6 CLIPACRRNHK 16
 1 CYIQNCPGCK 11

JLT 23

Q86V63 PRELIMINARY; PRT; 17 AA.

01-JUN-2003 (T-EMBLrel. 24, Created)

01-JUN-2003 (T-EMBLrel. 24, Last sequence update)

01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

Thyroid hormone beta 1 receptor (Fragment).

HTK<BETA>1.

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

[1]

SEQUENCE FROM N.A.
 MEDLINE=96064785; PubMed=7593432;

Ozata M., Suzuki S., Takeda T., Malkin D.G., Miyamoto T., Liu R.T.,
 Suzuki N., Silverberg J.D., Daneman D., Degroot L.J.;
 "Functional analysis of a proline to serine mutation in codon 453 of
 the thyroid hormone receptor beta 1 gene";
 J. Clin. Endocrinol. Metab. 80:3239-3245(1995).

EMBL; S80765; AAP32229.1; -

GO: GO:0004872; F:receptor activity; IEA.

Receptor.

NON_TER 1

NON_TER 17

SEQUENCE 17 AA; 1993 MW; 2CD7D41F852AB9D1 CRC64;

Query Match 19.5%; Score 24; DB 4; Length 17;

Best Local Similarity 42.9%; Pred. No. 5.8e+03;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

2 NWRCLLI 8

4 SWKCSRI 10

ULT 24

4C4

Q8B4C4 PRELIMINARY; PRT; 17 AA.

01-MAR-2003 (T-EMBLrel. 23, Created)

01-MAR-2003 (T-EMBLrel. 23, Last sequence update)

01-MAR-2003 (T-EMBLrel. 23, Last annotation update)

Precore.

Hepatitis B virus.

Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

NCBI_TaxID=10407;

[1]

SEQUENCE FROM N.A.

Vaishali C., Acharya S.K., Panda S.K.;

"Cryptic Hepatitis B virus infection: analysis of the complete genomic
 sequence of HBV from nine patients with seronegative viral

RT hepatitis";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY161158; AAO12630.1; -
 SQ SEQUENCE 17 AA; 1908 MW; 0B63A9BF82802588 CRC64;

Query Match 19.5%; Score 24; DB 12; Length 17;
 Best Local Similarity 66.7%; Pred. No. 5.8e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 CLIPAC 11

DB 7 CLIIIC 12

RESULT 25

O78379

ID O78379 PRELIMINARY; PRT; 18 AA.

AC O78379;

DT 01-NOV-1998 (T-EMBLrel. 08, Created)

DT 01-NOV-1998 (T-EMBLrel. 08, Last sequence update)

DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)

DE Small ribosomal protein S12 (Fragment).

GN RPS12.

OS Theileria annulata.

OG Chloroplast.

OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;

OC Theileria.

OX NCBI_TaxID=5874;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Hissar;

RA Denny P., Preiser P., Williamson D., Wilson I.;

"Evidence for a single origin of the 35 kb plastid DNA in

RT Apicomplexans";

RL Protist 149:51-59(1998).

DR EMBL; Y11429; CAA72235.1; -

DR GO: GO:0009507; C:chloroplast; IEA.

DR GO: GO:0003735; F:structural constituent of ribosome; IEA.

KW Chloroplast; Ribosomal protein.

FT NON_TER 1

SQ SEQUENCE 18 AA; 2331 MW; BBFFCC6E3C6037A CRC64;

Query Match 19.5%; Score 24; DB 8; Length 18;

Best Local Similarity 60.0%; Pred. No. 6.1e+03;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 15 HKKFC 19

DB 14 YKKYC 18

RESULT 26

Q9UWM9

ID Q9UWM9 PRELIMINARY; PRT; 19 AA.

AC Q9UWM9;

DT 01-MAY-2000 (T-EMBLrel. 13, Created)

DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (T-EMBLrel. 13, Last annotation update)

DE Arginine vasopressin-neurophysin II (Fragment).

GN AVP.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91123474; PubMed=1840604;

RA Ito M., Mori Y., Oiso Y., Saito H.;

"A single base substitution in the coding region for neurophysin II

RT associated with familial central diabetes insipidus.";

RL J. Clin. Invest. 87:725-728(1991).

DR EMBL; M63733; AAA69844.1; -

FT NON_TER 19

```
SEQUENCE 19 AA; 1985 MW; 5PF5PCD7BD990451 CRC64;
Query Match 19.5%; Score 24; DB 4; Length 19;
Best Local Similarity 60.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

7 LIPAC 11
:||||
:||||
5 MLPAC 9

CLT 27
MB5
Q9XMB5 PRELIMINARY; PRT; 19 AA.
Q9XMB5;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 12, Last annotation update)
ORF165 (Fragment).
Aegilops tauschii (Tausch's goatgrass) (Aegilops squarrosa).
Mitochondrion.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
Triticeae; Aegilops.
NCBI_TaxID=37682;
[1]
SEQUENCE FROM N.A.
STRAIN=KU29;
Tsukamoto N., Asakura N., Takumi S., Mori N., Nakamura C.;
"The presence of paternal sub-genomic mitochondrial DNA copies in the
nucleus-cytoplasm hybrids of tetraploid wheat with the cytoplasm of
Aegilops squarrosa.";
Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
EMBL; AF142479; AAD37354.1; -.
GO; GO:0005739; C:mitochondrion; IEA.
InterPro; IPR003319; YMF19.
Pfam; PF02326; YMF19; 1.
NON TER 19
SEQUENCE 19 AA; 2394 MW; F435DB3B595D3ADC CRC64;
Query Match 19.5%; Score 24; DB 4; Length 19;
Best Local Similarity 57.1%; Pred. No. 6.4e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 FNRCCCL 7
13 FFWICLL 19

MULT 28
1577
Q88577 PRELIMINARY; PRT; 12 AA.
Q88577;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Theiler's murine encephalomyelitis virus 5' flank and 5' end cds
(Fragment).
Theiler's encephalomyelitis virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
Cardiovirus.
NCBI_TaxID=12124;
[1]
SEQUENCE FROM N.A.
MEDLINE=92194426; PubMed=1548749;
Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
"A single base deletion in the 5' noncoding region of Theiler's virus
attenuates neurovirulence.";
J. Virol. 66:1951-1958(1992).
EMBL; M80885; AAA73156.1; -.
NON TER 12
```

```
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;
Query Match 18.7%; Score 23; DB 12; Length 12;
Best Local Similarity 30.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 10 ACRNHKKFC 19
|||||
|:|
Db 2 ACKHGYDVC 11

RESULT 29
Q88578 PRELIMINARY; PRT; 12 AA.
Q88578;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Theiler's murine encephalomyelitis virus 5' flank and 5' end cds
(Fragment).
Theiler's encephalomyelitis virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
Cardiovirus.
NCBI_TaxID=12124;
[1]
SEQUENCE FROM N.A.
STRAIN=TO(B15);
RC MEDLINE=92194426; PubMed=1548749;
Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
"A single base deletion in the 5' noncoding region of Theiler's virus
attenuates neurovirulence.";
J. Virol. 66:1951-1958(1992).
DR EMBL; M80886; AAA73157.1; -.
FT NON TER 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;
Query Match 18.7%; Score 23; DB 12; Length 12;
Best Local Similarity 30.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 10 ACRNHKKFC 19
|||||
|:|
Db 2 ACKHGYDVC 11

RESULT 30
Q88579 PRELIMINARY; PRT; 12 AA.
Q88579;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Theiler's murine encephalomyelitis virus 5' flank and 5' end cds
(Fragment).
Theiler's encephalomyelitis virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
Cardiovirus.
NCBI_TaxID=12124;
[1]
SEQUENCE FROM N.A.
STRAIN=VL;
RC MEDLINE=92194426; PubMed=1548749;
Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
"A single base deletion in the 5' noncoding region of Theiler's virus
attenuates neurovirulence.";
J. Virol. 66:1951-1958(1992).
DR EMBL; M80887; AAA73158.1; -.
FT NON TER 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;
Query Match 18.7%; Score 23; DB 12; Length 12;
Best Local Similarity 30.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 10 ACRNHKKFC 19
|||||
|:|
Db 2 ACKHGYDVC 11
```

10 ACRNHKKFC 19
||: :
2 ACKGYDVC 11

UT 31

575 PRELIMINARY; PRT; 12 AA.

Q88575
01-NOV-1996 (TReMBLrel. 01, Created)
01-NOV-1996 (TReMBLrel. 01, Last sequence update)
01-DEC-2001 (TReMBLrel. 19, Last annotation update)
Theiler's murine encephalomyelitis virus 5' flank and 5' end cds
(Fragment).
Theiler's encephalomyelitis virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
Cardiovirus.
NCBI_TaxID=12124;
[1]
SEQUENCE FROM N.A.
STRAIN=FA;
MEDLINE=92194426; PubMed=1548749;
Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
"A single base deletion in the 5' noncoding region of Theiler's virus
attenuates neurovirulence."
J. Virol. 66:1951-1958(1992).
EMBL; M80883; AAA73154.1; -.
NON TER 12 12
SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 18.7%; Score 23; DB 12; Length 12;

Best Local Similarity 30.0%; Pred. No. 6.2e+03;

Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

10 ACRNHKKFC 19

||: :
2 ACKGYDVC 11

UT 32

580 PRELIMINARY; PRT; 12 AA.

Q88580;
01-NOV-1996 (TReMBLrel. 01, Created)
01-NOV-1996 (TReMBLrel. 01, Last sequence update)
01-DEC-2001 (TReMBLrel. 19, Last annotation update)
Theiler's murine encephalomyelitis virus 5' flank and 5' end cds
(Fragment).
Theiler's encephalomyelitis virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
Cardiovirus.
NCBI_TaxID=12124;
[1]
SEQUENCE FROM N.A.
STRAIN=Vilyuski;
MEDLINE=92194426; PubMed=1548749;
Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
"A single base deletion in the 5' noncoding region of Theiler's virus
attenuates neurovirulence."
J. Virol. 66:1951-1958(1992).
EMBL; M80888; AAA73159.1; -.
NON TER 12 12
SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 18.7%; Score 23; DB 12; Length 12;

Best Local Similarity 30.0%; Pred. No. 6.2e+03;

Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

10 ACRNHKKFC 19

||: :
2 ACKGYDVC 11

RESULT 33

Q88582 PRELIMINARY; PRT; 12 AA.

AC Q88582;
01-NOV-1996 (TReMBLrel. 01, Created)
01-NOV-1996 (TReMBLrel. 01, Last sequence update)
01-DEC-2001 (TReMBLrel. 19, Last annotation update)
Theiler's murine encephalomyelitis virus 5' flank and 5' end cds
(Fragment).
Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
NCBI_TaxID=12124;
[1]
SEQUENCE FROM N.A.
STRAIN=TO(Vale);
MEDLINE=92194426; PubMed=1548749;
Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
"A single base deletion in the 5' noncoding region of Theiler's virus
attenuates neurovirulence."
J. Virol. 66:1951-1958(1992).
EMBL; M80890; AAA73161.1; -.
NON TER 12 12
SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 18.7%; Score 23; DB 12; Length 12;

Best Local Similarity 30.0%; Pred. No. 6.2e+03;

Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 10 ACRNHKKFC 19

||: :
2 ACKGYDVC 11

RESULT 34

Q88581 PRELIMINARY; PRT; 12 AA.

AC Q88581;
01-NOV-1996 (TReMBLrel. 01, Created)
01-NOV-1996 (TReMBLrel. 01, Last sequence update)
01-DEC-2001 (TReMBLrel. 19, Last annotation update)
Theiler's murine encephalomyelitis virus 5' flank and 5' end cds
(Fragment).
Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
NCBI_TaxID=12124;
[1]
SEQUENCE FROM N.A.
STRAIN=WW;
MEDLINE=92194426; PubMed=1548749;
Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
"A single base deletion in the 5' noncoding region of Theiler's virus
attenuates neurovirulence."
J. Virol. 66:1951-1958(1992).
EMBL; M80889; AAA73160.1; -.
NON TER 12 12
SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 18.7%; Score 23; DB 12; Length 12;

Best Local Similarity 30.0%; Pred. No. 6.2e+03;

Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 10 ACRNHKKFC 19

||: :
2 ACKGYDVC 11

RESULT 35

Q88576 PRELIMINARY; PRT; 12 AA.

ID Q88576
AC Q88576;

01-NOV-1996 (TRENBLrel. 01, Created)
01-NOV-1996 (TRENBLrel. 01, Last sequence update)
01-DEC-2001 (TRENBLrel. 19, Last annotation update)
Theiler's murine encephalomyelitis virus 5' flank and 5' end cds
(Fragment).
Theiler's encephalomyelitis virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
Cardiovirus.
NCBI_TaxID=12124;
[1]
SEQUENCE FROM N.A.
STRAIN=MHG;
MEDLINE=92194426; PubMed=1548749;
Pritchard A.E., Calenoff M.A, Simpson S., Jensen K., Lipton H.L.;
"A single base deletion in the 5' noncoding region of Theiler's virus
attenuates neurovirulence."
J. Virol. 66:1951-1958(1992).
EMBL; M80884; AAA73155.1; -.
NON TER 12
SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;
Query Match 18.7%; Score 23; DB 12; Length 12;
Best Local Similarity 30.0%; Pred.No. 6.2e+03;
Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
10 ACRNHHKFC 19
|||:
2 ACKGYDVC 11
arch completed: February 18, 2004, 06:28:48
; time : 40 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

protein - protein search, using sw model

1 on: February 18, 2004, 06:08:09 ; Search time 52 seconds
(without alignments)
103.239 Million cell updates/sec

le: US-09-806-376-1
fect score: 123
quence: 1 FNRCLIPACRRHKKFC 19

bring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

arched: 1586107 seqs, 282547505 residues

tal number of hits satisfying chosen parameters: 490463

nimum DB seq length: 0
ximum DB seq length: 19

st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

tabase :
1: Geneseqp29Jan04: *
2: Geneseqp1980s: *
3: Geneseqp1990s: *
4: Geneseqp2000s: *
5: Geneseqp2001s: *
6: Geneseqp2002s: *
7: Geneseqp2003s: *
8: Geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	Query Match	Length	DB	ID	Description
1	123	100.0	19	3	AA92227	AA92227 Rho-conotoxin
2	95	77.2	15	3	AA92228	AA92228 Truncated
3	50	40.7	18	2	AA92280	AA92280 A-lineage
4	50	40.7	18	2	AA92242	AA92242 A-lineage
5	49	39.8	16	2	AA92527	AA92527 A-lineage
6	49	39.8	16	2	AA92486	AA92486 Predatory
7	49	39.8	16	2	AA92737	AA92737 A-lineage
8	49	39.8	16	5	ABP60018	ABP60018 Alpha-con
9	49	39.8	17	5	ABG99820	ABG99820 Conus sp
10	49	39.8	18	3	AB21436	AB21436 Cone snail
11	48	39.0	16	2	AA92415	AA92415 A-lineage
12	48	39.0	18	2	AA92487	AA92487 Predatory
13	48	39.0	18	3	AA92522	AA92522 Mature co
14	48	39.0	18	3	AA92523	AA92523 Cone snail
15	47	38.2	16	2	AA92415	AA92415 A-lineage
16	47	38.2	17	3	AA92158	AA92158 Alpha-con
17	46	37.4	18	2	AA92529	AA92529 A-lineage
18	46	37.4	18	2	AA92487	AA92487 Predatory
19	46	37.4	18	2	AA92751	AA92751 A-lineage
20	45	36.6	16	5	ABG99823	ABG99823 Conus sp
21	45	36.6	18	3	AA92520	AA92520 Mature co
22	44	35.8	16	2	AA92527	AA92527 A-lineage
23	44	35.8	16	2	AA92486	AA92486 Predatory
24	44	35.8	16	2	AA92489	AA92489 Predatory
25	44	35.8	16	2	AA92741	AA92741 A-lineage

26	44	35.8	16	2	AA92753	AA92753 A-lineage
27	44	35.8	16	2	AA92790	AA92790 Conotoxin
28	44	35.8	16	2	AA92416	AA92416 Alpha-con
29	44	35.8	16	2	AA92520	AA92520 Alpha-con
30	44	35.8	16	5	ABG99827	ABG99827 Conus sp
31	44	35.8	16	6	ABP60014	ABP60014 Alpha-con
32	44	35.8	17	2	AA92415	AA92415 A-lineage
33	44	35.8	17	5	ABG99818	ABG99818 Conus sp
34	44	35.8	17	5	ABG99833	ABG99833 Conus sp
35	44	35.8	17	5	ABG99817	ABG99817 Conus sp
36	44	35.8	17	5	ABG99825	ABG99825 Conus sp
37	44	35.8	19	2	AA92528	AA92528 A-lineage
38	44	35.8	19	2	AA92743	AA92743 A-lineage
39	44	35.8	19	3	AA92465	AA92465 Amino aci
40	44	35.8	19	3	AA92465	AA92465 Amino aci
41	43	35.0	16	2	AA92527	AA92527 A-lineage
42	43	35.0	16	2	AA92488	AA92488 Predatory
43	43	35.0	16	2	AA92736	AA92736 A-lineage
44	43	35.0	16	2	AA92415	AA92415 Alpha-con
45	43	35.0	19	5	ABP60156	ABP60156 Gamma-car
46	43	35.0	19	5	ABP60167	ABP60167 Core snail
47	43	35.0	19	5	ABP88438	ABP88438 C marmore
48	42	34.1	16	2	AA92416	AA92416 Alpha-con
49	42	34.1	16	2	AA92415	AA92415 Alpha-con
50	42	34.1	16	5	AA92084	AA92084 Conus pen

ALIGNMENTS

RESULT 1
AA92227
ID AA92227 standard; peptide; 19 AA.
XX
AC AA92227;
XX
DT 10-AUG-2000 (first entry)
XX
DE Rho-conotoxin peptide, rho-TIA.
XX
KW Rho-conotoxin; alpha-1-adrenoreceptor; antagonist; hypotensive; cardiatic;
XX analgesic; antiarrhythmic; cytostatic; nootropic; antiinflammatory.
XX
OS Conus tulipa.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 5 /note= "involved in disulphide bond"
FT Disulfide-bond 6 /note= "involved in disulphide bond"
FT Disulfide-bond 11 /note= "involved in disulphide bond"
FT Disulfide-bond 19 /note= "involved in disulphide bond"
XX
WO200020443-A1.
13-APR-2000.
01-OCT-1999; 99WO-AU0000843.
02-OCT-1998; 98AU-00006273.
(UYQU) UNIV-QUEENSLAND.
Lewis RJ, Alewood PF, Sharpe IA;
WPI; 2000-303737/26.
Isolated rho-conotoxin peptide used for the treatment of urinary or
cardiovascular conditions or diseases, mood disorders or for control of
pain or inflammation comprises selective alpha1-adrenoreceptor antagonist
activity.

Claim 2; Page 31; 47pp; English.

The rho-conotoxin peptide, rho-TIA, is isolated from the venom duct of the fish hunting cone snail Conus tulipa. It contains two disulphide bonds. The rho-conotoxin peptide has selective alpha-1-adrenoceptor antagonist activity. It can be used in a receptor binding assay to test the activity of a molecule as an antagonist of alpha-1-adrenoceptor activity. Rho-TIA is labeled, e.g. with radioactive isotope and used to identify molecules which act at the same site. Antibodies to rho-TIA are useful as therapeutic and diagnostic agents. Rho-conotoxin can be used for the treatment of or prophylaxis of a urinary system disease, e.g. prostatic hyperplasia, cardiovascular disease, e.g. arrhythmia, hypertension or coronary heart failure, a mood disorder, e.g. craving (e.g. smoking craving) and pain, e.g. chronic pain, neuropathic pain or inflammatory pain (all claimed)

Sequence 19 AA;

Query Match 100.0%; Score 123; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.7e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 FNRWCLIPACRRNHKKFC 19
|||||
1 FNRWCLIPACRRNHKKFC 19

SULT 2

Y92228
AA92228 standard; peptide; 15 AA.

AA92228;

10-AUG-2000 (first entry)

Truncated, inactive rho-conotoxin peptide derivative.

Rho-conotoxin; alpha-1-adrenoceptor; antagonist; hypotensive; cardiant; analgesic; antiarrhythmic; cytostatic; nootropic; antiinflammatory.

Conus tulipa.
Synthetic.

Key Location/Qualifiers
Disulfide-bond 5 /note= "involved in disulphide bond"
Disulfide-bond 6 /note= "involved in disulphide bond"
Disulfide-bond 11 /note= "involved in disulphide bond"
Disulfide-bond 19 /note= "involved in disulphide bond"

WO200020443-A1.

13-APR-2000.

01-OCT-1999; 99WO-AU000843.

02-OCT-1998; 98AU-00006273.

(UYQU) UNIV QUEENSLAND.

Lewis RJ, Alewood PF, Sharpe IA;

WPI; 2000-303737/26.

Isolated rho-conotoxin peptide used for the treatment of urinary or cardiovascular conditions or diseases, mood disorders or for control of pain or inflammation comprises selective alpha-1-adrenoceptor antagonist activity.

Disclosure; Page 3; 47pp; English.

The rho-conotoxin peptide, rho-TIA (see AA92227), is isolated from the venom duct of the fish hunting cone snail Conus tulipa. It contains two disulphide bonds. The rho-conotoxin peptide has selective alpha-1-adrenoceptor antagonist activity. It can be used in a receptor binding assay to test the activity of a molecule as an antagonist of alpha-1-adrenoceptor activity. Rho-TIA is labeled, e.g. with radioactive isotope and used to identify molecules which act at the same site. Antibodies to rho-TIA are useful as therapeutic and diagnostic agents. Rho-conotoxin can be used for the treatment of or prophylaxis of a urinary system disease, e.g. prostatic hyperplasia, cardiovascular disease, e.g. arrhythmia, hypertension or coronary heart failure, a mood disorder, e.g. craving (e.g. smoking craving) and pain, e.g. chronic pain, neuropathic pain or inflammatory pain (all claimed)

Sequence 15 AA;

Query Match 77.2%; Score 95; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19
|||||
DB 1 CCLIPACRRNHKKFC 15

RESULT 3

AA92228
ID AAR75280 standard; peptide; 18 AA.

AC AAR75280;

DT 22-DEC-1995 (first entry)

DE A-lineage conotoxin SL-1 peptide.

KW Alpha conotoxin; neuromuscular; synapse; signal transmission.

OS Conus sulcatus.

FH Key Location/Qualifiers
FT Misc-difference 7 /label= Pro or OTHER
FT /note= "Hydroxyproline"

FT Misc-difference 14 /label= Pro or OTHER
FT /note= "Hydroxyproline"

FT Modified-site 15 /note= "Glu, can form a peptide bond via either the alpha
or gamma carboxyl group"

FT Modified-site 18 /note= "preferably amidated"

XX WO9511256-A1.

XX 27-APR-1995.

XX 19-OCT-1994; 94WO-US011927.

XX 19-OCT-1993; 93US-00137800.

XX (UTAH) UNIV UTAH RES FOUND.

XX Olivera BM, Cruz LJ, Hillyard DR, McIntosh JM, Santos AD;

XX WPI; 1995-170189/22.

XX New A-lineage conotoxin peptide(s) - which inhibit synaptic transmission at the neuromuscular junction or are active against potassium or sodium channels.

XX Claim 1; Page 44; 66pp; English.

The kappa-conotoxin, alpha conotoxin and alpha-like conotoxin peptides all belong to a group of peptides known as the A-lineage conotoxin peptides. The A lineage conotoxin peptides have a wide variety of pharmacological uses. The A-lineage conotoxin peptides claimed (AAR75264-R75293) are useful for the inhibition of synaptic transmission at neuromuscular junctions by blocking nicotinic acetyl choline receptors and they also have activity against voltage-gated Na and K channels

Sequence 18 AA;
Query Match 40.7%; Score 50; DB 2; Length 18;
Best Local Similarity 46.7%; Pred. No. 11;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
5 CCLIPACRRNHKKFC 19
||| ||||| :
3 CCSFPACKYRPEMC 17

SULT 4
W12742
AAW12742 standard; peptide; 18 AA.
AAW12742;
25-MAR-2003 (revised)
16-APR-1997 (first entry)
A-lineage conotoxin peptide SL-1.

Polymerase chain reaction; PCR; primer; amplify; conotoxin; Conus; inhibitor; synaptic transmission; neuromuscular junction; sodium channel; nicotinic acetylcholine receptor; potassium channel; muscle relaxant; myasthenia gravis; small cell lung cancer; therapy.
Conus sulcatus.

Key Location/Qualifiers
Modified-site 7 /note= "optionally hydroxylated"
Modified-site 14 /note= "optionally hydroxylated"
Modified-site 15 /note= "optionally gamma-carboxylated"
Modified-site 18 /note= "amidated"

US5589340-A.
31-DEC-1996.
07-JUN-1995; 95US-00477383.
29-JUN-1993; 93US-00084848.
19-OCT-1993; 93US-00137800.
(UTAH) UNIV UTAH RES FOUND.
Santos AD, Hillyard DR, McIntosh JM, Olivera BM, Cruz LJ;
WPI; 1997-076840/07.

Identifying nucleic acid encoding A-lineage conotoxin peptide(s) by amplification - uses primers corresponding to conserved regions in the signal sequence and 3'-untranslated regions, useful e.g. in treatment of small cell lung cancer.

Disclosure; Col 5; 36pp; English.
AAW12726-W12769 represent conotoxin peptides. This sequence represents the A-lineage conotoxin SL-1 peptide isolated from Conus sulcatus. These sequences are identified using the method of the invention. The method of

the invention is for identifying DNA encoding A-lineage conotoxin peptides by subjecting Conus nucleic acid to amplification with primer sequences (see AAT59714 and AAT59715). The primers are specific for the signal sequence and 3'-untranslated (3'UTR) regions of the conotoxin gene, which are highly homologous between conotoxins, and are therefore suitable sites for detection. A-lineage conotoxins include alpha-conotoxins, and kappa-conotoxins. Alpha-conotoxins are powerful inhibitors of synaptic transmission at the neuromuscular junction, and are usually nicotinic acetylcholine receptor blockers. Kappa-conotoxins act on the voltage sensitive sodium and potassium channels. The conotoxins identified can be used as muscle relaxants, in the diagnosis of myasthenia gravis, and for the treatment or diagnosis of small cell lung cancer. For the treatment of small cell lung cancer, the conotoxin peptides act by binding to the nicotinic receptors, and thereby blocking the nicotine/cytosine stimulated release of the mitogen 5-hydroxytryptamine. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 18 AA;

Query Match 40.7%; Score 50; DB 2; Length 18;
Best Local Similarity 46.7%; Pred. No. 11;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 5 CCLIPACRRNHKKFC 19
||| ||||| :
DB 3 CCSFPACKYRPEMC 17

RESULT 5
AAR75275
ID AAR75275 standard; peptide; 16 AA.
XX
AC AAR75275;
XX
DT 27-AUG-2003 (revised)
DT 21-DEC-1995 (first entry)
XX
DE A-lineage conotoxin BN-2 peptide.
XX
KW Conotoxin; neuromuscular; synapse; signal transmission; inhibitor.
XX
OS Conus bandanus.

Key Location/Qualifiers
FT Misc-difference 6 /label= Pro or OTHER
FT /note= "Hydroxyproline"
FT Misc-difference 13 /label= Pro or OTHER
FT /note= "Hydroxyproline"
FT Modified-site 16 /note= "preferably amidated"
FT
PN WO9511256-A1.
XX
XX 27-APR-1995.
PD
XX 19-OCT-1994; 94WO-US011927.
XX
XX 19-OCT-1993; 93US-00137800.
XX (UTAH) UNIV UTAH RES FOUND.
XX

PI Olivera BM, Cruz LJ, Hillyard DR, McIntosh JM, Santos AD;
XX
XX WPI; 1995-170189/22.
DR
XX New A-lineage conotoxin peptide(s) - which inhibit synaptic transmission at the neuromuscular junction or are active against potassium or sodium channels.
PT
XX Claim 1; Page 42; 66pp; English.
XX
XX

The kappa-conotoxin, alpha conotoxin and alpha-like conotoxin peptides all belong to a group of peptides known as the A-lineage conotoxin peptides. The A-lineage conotoxin peptides have a wide variety of pharmacological uses. The A-lineage conotoxin peptides claimed (AAR75264-R75293) are useful for the inhibition of synaptic transmission at neuromuscular junctions by blocking nicotinic acetyl choline receptors and they also have activity against voltage-gated Na and K channels. (Updated on 27-AUG-2003 to correct OS field.)

Sequence 16 AA;

Query Match 39.8%; Score 49; DB 2; Length 16;
Best Local Similarity 46.7%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19
||| ||| :| :|
2 CCTHPACHVSHPELC 16

RESULT 6

AAW24882
AAW24882 standard; peptide; 16 AA.

AAW24882;

25-MAR-2003 (revised)
15-OCT-1997 (first entry)

Predatory cone snail venom alpha-conotoxin BN-2.

Conotoxin; venom; predatory; cone snail; Conus; A-lineage; inhibitor; synaptic transmission; neuromuscular junction; block; alpha-conotoxin; nicotinic acetylcholine receptor; kappa-conotoxin; voltage-sensitive potassium CHANNEL; sodium channel.

Conus bandanus.

Key	Location/Qualifiers
Modified-site 6	/note= "optionally may be 4Hyp"
Modified-site 13	/note= "optionally may be 4Hyp"
Modified-site 16	/note= "amidated C-terminus"

US5633347-A.

27-MAY-1997.

07-JUN-1995; 95US-00480750.

29-JUN-1993; 93US-00084848.

19-OCT-1993; 93US-00137800.

(UTAH) UNIV UTAH RES FOUND.

Hillyard DR, Cruz LJ, McIntosh JM, Santos AO, Olivera BM;

WPI; 1997-309336/28.

New kappa-conotoxin peptide(s) - present in venom of fish-hunting cone snail.

Disclosure; Col 5; 37pp; English.

The peptides AAW24878-W24900 represent novel toxin peptides isolated from the venom of various predatory cone snails of the genus Conus. The peptides are A-lineage conotoxin peptides which fall into 3 groups dependent on their amino acid sequences: (i) alpha-3/5 have a core sequence CCXXCCXXCC where X is any amino acid; (ii) alpha-4/7 have a core sequence CCXXCCXXCCXXCC; and (iii) kappa-7/2/1/3 have the core sequence CCXXCCXXCCXXCCXXCC. The peptide presented here was isolated

CC from Conus bandanus and falls into the alpha-4/7 category. Alpha-conotoxin peptides are potent inhibitors of synaptic transmission at the neuromuscular junction by blocking nicotinic acetylcholine receptors, CC whereas kappa-conotoxins have activities against voltage-sensitive CC potassium or sodium channels. (Updated on 25-MAR-2003 to correct PF CC field.)

XX SQ Sequence 16 AA;

Query Match 39.8%; Score 49; DB 2; Length 16;
Best Local Similarity 46.7%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19
||| ||| :| :|
Db 2 CCTHPACHVSHPELC 16

RESULT 7

AAW12737
ID AAW12737 standard; peptide; 16 AA.

XX AAW12737;

XX 25-MAR-2003 (revised)

DT 16-APR-1997 (first entry)

XX A-lineage conotoxin peptide BN-2.

XX Polymerase chain reaction; PCR; primer; amplify; conotoxin; Conus; KW inhibitor; synaptic transmission; neuromuscular junction; sodium channel; KW nicotinic acetylcholine receptor; potassium channel; muscle relaxant; KW myasthenia gravis; small cell lung cancer; therapy.

XX Conus bandanus.

Key	Location/Qualifiers
Modified-site 6	/note= "optionally hydroxylated"
Modified-site 13	/note= "optionally hydroxylated"
Modified-site 15	/note= "amidated"

US5589340-A.

31-DEC-1996.

07-JUN-1995; 95US-00477383.

29-JUN-1993; 93US-00084848.

19-OCT-1993; 93US-00137800.

(UTAH) UNIV UTAH RES FOUND.

Santos AD, Hillyard DR, McIntosh JM, Olivera BM, Cruz LJ;

WPI; 1997-076840/07.

Identifying nucleic acid encoding A-lineage conotoxin peptide(s) by amplification - uses primers corresponding to conserved regions in the signal sequence and 3'-untranslated regions, useful e.g. in treatment of small cell lung cancer.

Disclosure; Col 5; 36pp; English.

AAW12725-W12769 represent conotoxin peptides. This sequence represents the A-lineage conotoxin BN-2 peptide isolated from Conus bandanus. These sequences are identified using the method of the invention. The method of the invention is for identifying DNA encoding A-lineage conotoxin peptides by subjecting Conus nucleic acid to amplification with primer sequences (see AAR59714 and AAR59715). The primers are specific for the signal sequence and 3'-untranslated (3'UTR) regions of the conotoxin

New alpha-conotoxin-like peptides that inhibit the activity of neuronal nicotinic acetylcholine receptor, useful for treating stroke, pain, schizophrenia, Parkinson's disease, small cell lung carcinoma or Alzheimer's disease.

XX This invention describes novel conotoxin peptides from the cone snail, CC CC genus *Conus* which have analgesic activity and can act as a voltage-gated CC CC

ion channel modulator or a ligand-gated ion channel modulator. The conotoxin peptide is useful as a pain-relieving agent for alleviating pain in an individual who is either exhibiting pain or is about to be subjected to a pain-causing event. The conotoxin peptide is also useful for treating or preventing disorders associated with voltage-gated ion channel disorders, ligand-gated ion channel disorders or receptor disorders. The radiolabeled conotoxin peptide is also useful for characterizing a new site on these receptors or channels, and for screening and identifying novel small molecules that interact with the above-mentioned channels or receptors, which are monoamine transporters. ABG9360-ABG9983 represent the conotoxin protein and peptides described in the disclosure of the invention

Sequence 17 AA;

Query Match 39.8%; Score 49; DB 5; Length 17;

Best Local Similarity 46.7%; Pred. No. 14;

Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19

3 CCTHPACHVSHPELC 17

RESULT 10

AB21436

AAB21436 standard; peptide; 18 AA.

AAB21436;

19-JAN-2001 (first entry)

Cone snail alpha-conotoxin SEQ ID NO: 79.

Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder; neuronal nicotinic acetylcholine receptor; cardiovascular disorder; gastric motility disorder; urinary incontinence; nicotine addiction; small cell lung carcinoma.

Conus bandanus.

WO200044776-A1.

03-AUG-2000.

28-JAN-2000; 2000WO-US001979.

29-JAN-1999; 99US-0118381P.

(UTAH) UNIV UTAH RES FOUND.

(COGN-) COGNETIX INC.

Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

WPI; 2000-505965/45.

N-PSDB; AAA89411.

alpha-conotoxin polypeptides derived from the venom of cone snails useful e.g. as neuromuscular blocking agents for use in surgery and for treating unipolar depression.

Claim 39; Page 34; 229pp; English.

The present invention relates to a number of alpha-conotoxin peptides and their coding sequences from a number of different species of cone snail. These peptides are found in minute quantities in the venom of the snails, and are targeted at the neuronal nicotinic acetylcholine receptors of the nervous system. They usually contain two disulphide bonds, which give them defined conformations, a rarity in molecules this small. The alpha-conotoxins can be used as neuromuscular blocking agents in surgery, and for treating disorders regulated at the neuronal nicotinic acetylcholine receptors, including cardiovascular disorders, gastric motility disorders, urinary incontinence, nicotine addiction, mood disorders such

CC as bipolar disorder, unipolar depression, dysthymia and seasonal
CC affective disorder, and small cell lung carcinoma

XX Sequence 18 AA;

Query Match 39.8%; Score 49; DB 3; Length 18;

Best Local Similarity 46.7%; Pred. No. 14;

Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19

3 CCTHPACHVSHPELC 17

RESULT 11

AAV24163

ID AAY24163 standard; peptide; 16 AA.

AC AAY24163;

DT 10-SEP-1999 (first entry)

XX Alpha-conotoxin peptide SEQ ID NO:9.

Alpha-conotoxin; neuronal nicotinic acetylcholine receptor; nAChR; small cell lung carcinoma; cardiovascular disorder; nicotine addiction; gastric motility disorder; urinary incontinence; mood disorder; bipolar disorder; unipolar depression; dysthymia; seasonal effective disorder.

Conus purpurascens.

WO9933482-A1.

08-JUL-1999.

23-DEC-1998; 98WO-US027367.

31-DEC-1997; 97US-0070153P.

03-APR-1998; 98US-0080588P.

(UTAH) UNIV UTAH RES FOUND.

Olivera BM, McIntosh JM, Yoshikami D, Cartier GE, Luo S;

WPI; 1999-405367/34.

Alpha-conotoxin peptides that are used to treat disorders regulated at neuronal nicotinic acetylcholine receptors.

Claim 28; Page 6; 40pp; English.

The present sequence represents a specifically claimed example of an alpha-conotoxin, which can be used to treat disorders regulated at neuronal nicotinic acetylcholine receptors (nAChR). The alpha-conotoxins are useful for preparing a pharmaceutical composition for treating disorders regulated at neuronal nAChR, especially alpha 3 beta 2, alpha 3 beta 4 or alpha 7-containing nAChR. Disorders that can be treated include cardiovascular disorders, a gastric motility disorder, urinary incontinence, nicotine addiction, a mood disorder or small cell lung carcinoma. Mood disorders include bipolar disorder, unipolar depression, dysthymia and seasonal effective disorder. The alpha-conotoxins can also be used for diagnosis of small cell lung carcinoma. The alpha-conotoxin antagonists are able to discriminate between non-symmetrical ligand binding interfaces present on the nAChR. The alpha-conotoxin has the ability to potentially block any receptor containing an alpha beta subunit interface, regardless of what other subunits may be present in the receptor complex

XX Sequence 16 AA;

Query Match 39.0%; Score 48; DB 2; Length 16;

Best Local Similarity 40.0%; Pred. No. 17;

atches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19
|||:|:|:
2 CCSLPFCAANNPDYC 16

ULT 12
424867

AAW24887 standard; peptide; 18 AA.

AAW24887;

25-MAR-2003 (revised)

15-OCT-1997 (first entry)

Predatory cone snail venom alpha-conotoxin SL-1.

Conotoxin; venom; predatory; cone snail; Conus; A-lineage; inhibitor;
synaptic transmission; neuromuscular junction; block; alpha-conotoxin;
nicotinic acetylcholine receptor; kappa-conotoxin;
voltage-sensitive potassium CHANNEL; sodium channel.

Conus sulcatus.

Key Location/Qualifiers

Modified-site 7 /note= "optionally 4Hyp"

Modified-site 14 /note= "optionally 4Hyp"

Misc-difference 15

/label= Glu, OTHER

/note= "OTHER = gamma-carboxyglutamate (Glu)"

Modified-site 18 /note= "amidated C-terminus"

US5633347-A.

27-MAY-1997.

07-JUN-1995; 95US-00480750.

29-JUN-1993; 93US-00084848.

19-OCT-1993; 93US-00137800.

(UTAH) UNIV UTAH RES FOUND.

Hillyard DR, Cruz LJ, McIntosh JM, Santos AO, Olivera BW;

WPI; 1997-309336/28.

New kappa-conotoxin peptide (s) - present in venom of fish-hunting cone snail.

Disclosure; Col 5; 37pp; English.

The peptides AAW24878-W4900 represent novel toxin peptides isolated from the venom of various predatory cone snails of the genus Conus. The peptides are A-lineage conotoxin peptides which fall into 3 groups dependent on their amino acid sequences: (i) alpha-3/5 have a core sequence CCXXCCXXXCC where X is any amino acid; (ii) alpha-4/7 have a core sequence CCXXXCCXXXCC; and (iii) kappa-7/2/1/3 have the core sequence CCXXXCCXXXCCXXXCC. The peptide presented here was isolated from Conus sulcatus and falls into the alpha-4/7 category. Alpha-conotoxin peptides are potent inhibitors of synaptic transmission at the neuromuscular junction by blocking nicotinic acetylcholine receptors, whereas kappa-conotoxins have activities against voltage-sensitive potassium or sodium channels. (Updated on 25-MAR-2003 to correct Pf field.)

Sequence 18 AA;

Query Match 39.0%; Score 48; DB 2; Length 18;

Best Local Similarity 46.7%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19
|||:|:|:
DB 3 CCSFPACRKYRPMXC 17

RESULT 13

AAV87522

ID AAV87522 standard; peptide; 18 AA.

XX AAV87522;

DT 18-JUL-2000 (first entry)

DE Mature conotoxin peptide #2.

KW Mature conotoxin; brocade cone shell; line cone shell; drug screening;
KW neuronal inhibitor; muscle inhibitor.

OS Conus sp.

PN CN1237584-A.

PD 08-DEC-1999.

PF 30-APR-1999; 99CN-00106070.

PR 30-APR-1999; 99CN-00106070.

PA (BIOL-) BIOLOGICAL ENG INST ACAD MILITARY MEDICI.

PI Lu B, Huang P;

DR WPI; 2000-351193/31.

Conotoxin peptide from brocade cone shells useful as analgesic.

Claim 1A; Page 2; 20pp; Chinese.

The invention relates to 14 novel mature conotoxin peptides from marine snails (Conus species); conotoxin precursor proteins; and cDNAs encoding the conotoxin precursors. The mature peptide sequences were discovered by obtaining conotoxin cDNA sequences from mRNA from the brocade cone shell (Conus textile) or the line cone shell (Conus striatus). The cDNA sequences were used to determine the conotoxin precursor protein sequences, and the sequences of the mature conotoxin peptides were inferred from the precursor sequences. The mature conotoxin peptides can be obtained via chemical synthesis or by in vitro gene expression. Conotoxins inhibit the function of neurons and muscle cells. Certain conotoxins interfere with synaptic transmission, while others act on muscle or at the neuromuscular junction. The 14 novel conotoxins have unique receptor specificity and affinity, so can be used as screening tools to identify new drugs. Conotoxin #11 (AAV87540) may be used for pain relief. Sequences AAV87420, AAV87522, AAV87524, AAV87526, AAV87528, AAV87530, AAV87532, AAV87534, AAV87536, AAV87538, AAV87540, AAV87542, AAV87544 and AAV87546 represent mature conotoxins #1-#14, respectively.

Sequence 18 AA;

Query Match 39.0%; Score 48; DB 3; Length 18;

Best Local Similarity 46.7%; Pred. No. 19;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19
|||:|:|:
DB 3 CCSHPACNVDHPEIC 17

RESULT 14

AAB21523

ID AAB21523 standard; peptide; 18 AA.

AAB21523;

22-JAN-2001 (first entry)

Cone snail alpha-conotoxin SEQ ID NO: 203.

Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
neural nicotinic acetylcholine receptor; cardiovascular disorder;
gastric motility disorder; urinary incontinence; nicotine addiction;
small cell lung carcinoma.

Conus muscus.

Key Location/Qualifiers

Misc-difference 2

/label= Lys, OTHER

/note= "N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys"

Misc-difference 12

/label= Lys, OTHER

/note= "N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys"

Misc-difference 14

/label= Pro, OTHER

/note= "hydroxy-Pro"

Misc-difference 16

/label= Tyr, OTHER

/note= "mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr"

W0200044776-A1.

03-AUG-2000.

28-JAN-2000; 2000WO-US001979.

29-JAN-1999; 99US-0118381P.

(UTAH) UNIV UTAH RES FOUND.

(COGN-) COGNETIX INC.

Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;

WPI; 2000-505965/45.

alpha-conotoxin polypeptides derived from the venom of cone snails useful
e.g. as neuromuscular blocking agents for use in surgery and for treating
unipolar depression.

Claim 21; Page 80; 229pp; English.

The present invention relates to a number of alpha-conotoxin peptides and
their coding sequences from a number of different species of cone snail.
These peptides are found in minute quantities in the venom of the snails,
and are targeted at the neuronal nicotinic acetylcholine receptors of the
nervous system. They usually contain two disulphide bonds, which give
them defined conformations, a rarity in molecules this small. The alpha-
conotoxins can be used as neuromuscular blocking agents in surgery, and
for treating disorders regulated at the neuronal nicotinic acetylcholine
receptors, including cardiovascular disorders, gastric motility
disorders, urinary incontinence, nicotine addiction, mood disorders such
as bipolar disorder, unipolar depression, dysthymia and seasonal
affective disorder, and small cell lung carcinoma

Sequence 18 AA;

Query Match 39.0%; Score 48; DB 3; Length 18;

Best Local Similarity 46.7%; Pred. No. 19;

Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRHHKKFC 19

||: ||| | |

Db 3 CCINDACRSXHXQC 17

RESULT 15

AAY24158

ID AAY24158 standard; peptide; 16 AA.

XX AC

XX AAY24158;

XX DT 10-SEP-1999 (first entry)

XX DE

XX Alpha-conotoxin peptide SEQ ID NO:10.

XX KW

Alpha-conotoxin; neuronal nicotinic acetylcholine receptor; nAChR;
small cell lung carcinoma; cardiovascular disorder; nicotine addiction;
gastric motility disorder; urinary incontinence; mood disorder;
bipolar disorder; unipolar depression; dysthymia;
seasonal effective disorder.

XX KW

XX Conus purpurascens.

XX OS Synthetic.

XX PN W09933482-A1.

XX PD 08-JUL-1999.

XX PF 23-DEC-1998; 98WO-US027367.

XX PR 31-DEC-1997; 97US-0070153P.

XX PR 03-APR-1998; 98US-0080588P.

XX XX

XX (UTAH) UNIV UTAH RES FOUND.

XX XX

XX PI Olivera BM, McIntosh JM, Yoshikami D, Cartier GE, Luo S;

XX DR WPI; 1999-405367/34.

XX Alpha-conotoxin peptides that are used to treat disorders regulated at
neural nicotinic acetylcholine receptors.
XX Claim 12; Page 27; 40pp; English.

The present sequence represents a specifically claimed example of an
alpha-conotoxin from the general formula given in AAY24155, which can be
used to treat disorders regulated at neuronal nicotinic acetylcholine
receptors (nAChR). The alpha-conotoxins are useful for preparing a
pharmaceutical composition for treating disorders regulated at neuronal
nAChR, especially alpha 3 beta 2, alpha 3 beta 4 or alpha 7-containing
nAChR. Disorders that can be treated include cardiovascular disorders, a
gastric motility disorder, urinary incontinence, nicotine addiction, a
mood disorder or small cell lung carcinoma. Mood disorders include
bipolar disorder, unipolar depression, dysthymia and seasonal effective
disorder. The alpha-conotoxins can also be used for diagnosis of small
cell lung carcinoma. The alpha-conotoxin antagonists are able to
discriminate between non-symmetrical ligand binding interfaces present on
the nAChR. The alpha-conotoxin has the ability to potentially block any
receptor containing a alpha beta subunit interface, regardless of what
other subunits may be present in the receptor complex

Sequence 16 AA;

Query Match 38.2%; Score 47; DB 2; Length 16;

Best Local Similarity 40.0%; Pred. No. 23;

Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 5 CCLIPACRHHKKFC 19

||: ||| | |

Db 2 CCCLPPCALNNPDYC 16

RESULT 16

AAB21548

ID AAB21548 standard; peptide; 17 AA.

```

AAE21548;
22-JAN-2001 (first entry)
Cone snail alpha-conotoxin SEQ ID NO: 228.
Cone snail; alpha-conotoxin; venom; disulphide bond; mood disorder;
neural nicotinic acetylcholine receptor; cardiovascular disorder;
gastric motility disorder; urinary incontinence; nicotine addiction;
small cell lung carcinoma.
Conus tulipa.
Key Location/Qualifiers
Misc-difference 6
/label= Pro, OTHER
/Note= "hydroxy-Pro"
WO200044776-A1.
03-AUG-2000.
28-JAN-2000; 2000WO-US001979.
29-JAN-1999; 99US-0118381P.
(UTAH ) UNIV UTAH RES FOUND.
(COGN-) COGNETIX INC.
Watkins M, Olivera BM, Hillyard DR, McIntosh JM, Jones RM;
WPI; 2000-505965/45.
alpha-conotoxin polypeptides derived from the venom of cone snails useful
e.g. as neuromuscular blocking agents for use in surgery and for treating
unipolar depression.
Claim 21; Page 82; 229pp; English.
The present invention relates to a number of alpha-conotoxin peptides and
their coding sequences from a number of different species of cone snail.
These peptides are found in minute quantities in the venom of the snails,
and are targeted at the neuronal nicotinic acetylcholine receptors of the
nervous system. They usually contain two disulphide bonds, which give
them defined conformations, a rarity in molecules this small. The alpha-
conotoxins can be used as neuromuscular blocking agents in surgery, and
for treating disorders regulated at the neuronal nicotinic acetylcholine
receptors, including cardiovascular disorders, gastric motility
disorders, urinary incontinence, nicotine addiction, mood disorders such
as bipolar disorder, unipolar depression, dysthymia and seasonal
affective disorder, and small cell lung carcinoma
Sequence 17 AA;
Query Match 39.28; Score 47; DB 3; Length 17;
Best Local Similarity 53.3%; Pred. No. 25;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
5 CCLIPACRRNHKKFC 19
||| ||| :||
2 CCSNXACLVNHRFC 16
RESULT 17
UR75292
) AAR75292 standard; peptide; 18 AA.
AAR75292;
22-DEC-1995 (first entry)
A-lineage conotoxin U008 peptide.

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XX Conotoxin; neuromuscular; synapse; signal transmission; inhibitor.
XX Conus ermineus.
XX Key Location/Qualifiers
XX Misc-difference 3
XX /label= Pro or OTHER
XX /note= "Hydroxyproline"
XX Modified-site 18
XX /note= "preferably amidated"
XX WO9511256-A1.
XX BN
XX PD 27-APR-1995.
XX PF 19-OCT-1994; 94WO-US011927.
XX PR 19-OCT-1993; 93US-00137800.
XX PA (UTAH ) UNIV UTAH RES FOUND.
XX PI Olivera BM, Cruz LJ, Hillyard DR, McIntosh JM, Santos AD;
XX WPI; 1995-170189/22.
XX New A-lineage conotoxin peptide(s) - which inhibit synaptic transmission
XX at the neuromuscular junction or are active against potassium or sodium
XX channels.
XX Claim 1; Page 49; 66pp; English.
XX The kappa-conotoxin, alpha conotoxin and alpha-like conotoxin peptides
XX all belong to a group of peptides known as the A-lineage conotoxin
XX peptides. The A-lineage conotoxin peptides have a wide variety of
XX pharmacological uses. The A-lineage conotoxin peptides claimed (AAR75264-
XX R75293) are useful for the inhibition of synaptic transmission at
XX neuromuscular junctions by blocking nicotinic acetyl choline receptors
XX and they also have activity against voltage-gated Na and K channels
XX Sequence 18 AA;
Query Match 37.4%; Score 46; DB 2; Length 18;
Best Local Similarity 46.7%; Pred. No. 35;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 5 CCLIPACRRNHKKFC 19
||| ||| :||
Db 4 CCSNPACNVNVPQIC 18
RESULT 18
AAW24897
ID AAW24897 standard; peptide; 18 AA.
XX AC AAW24897;
XX DT 25-MAR-2003 (revised)
XX DT 15-OCT-1997 (first entry)
XX DE Predatory cone snail venom alpha-conotoxin U008.
XX Conotoxin; venom; predatory; cone snail; Conus; A-lineage; inhibitor;
XX synaptic transmission; neuromuscular junction; block; alpha-conotoxin;
XX nicotinic acetylcholine receptor; kappa-conotoxin;
XX voltage-sensitive potassium CHANNEL; sodium channel.
XX Conus ermineus.
XX Key Location/Qualifiers
XX Modified-site 3
XX /note= "optionally may be 4Hyp"
XX Modified-site 18

```

/note= "amidated C-terminus"

US5633347-A.

27-MAY-1997.

07-JUN-1995; 95US-00480750.

29-JUN-1993; 93US-00084848.

19-OCT-1993; 93US-00137800.

(UTAH) UNIV UTAH RES FOUND.

Hillyard DR, Cruz LJ, McIntosh JM, Santos AO, Olivera BM;

WPI; 1997-309336/28.

New kappa-conotoxin peptide(s) - present in venom of fish-hunting cone snail.

Disclosure; Col 6; 37pp; English.

The peptides AAW24878-W24900 represent novel toxin peptides isolated from the venom of various predatory cone snails of the genus *Conus*. The peptides are A-lineage conotoxin peptides which fall into 3 groups dependent on their amino acid sequences: (i) alpha-3/5 have a core sequence CXXXCXXXXC where X is any amino acid, (ii) alpha-4/7 have a core sequence CXXXCXXXCXXXC, and (iii) kappa-7/21/3 have the core sequence CXXXCXXXCXXXCXXXC. The peptide presented here was isolated from *Conus ermineus* and falls into the alpha-4/7 category. Alpha-conotoxin peptides are potent inhibitors of synaptic transmission at the neuromuscular junction by blocking nicotinic acetylcholine receptors, whereas kappa-conotoxins have activities against voltage-sensitive potassium or sodium channels. (Updated on 25-MAR-2003 to correct PF field.)

Sequence 18 AA;

Query Match 37.4%; Score 46; DB 2; Length 18;

Best Local Similarity 46.7%; Pred. No. 35;

Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19

4 CCSNPACNVNPPQIC 18

RESULT 19

AAW12751 standard; peptide; 18 AA.

AAW12751;

27-AUG-2003 (revised)

25-MAR-2003 (revised)

16-APR-1997 (first entry)

A-lineage conotoxin peptide U008.

Polymerase chain reaction; PCR; primer; amplify; conotoxin; *Conus*; inhibitor; synaptic transmission; neuromuscular junction; sodium channel; nicotinic acetylcholine receptor; potassium channel; muscle relaxant; myasthenia gravis; small cell lung cancer; therapy.

Conus ermineus.

Key Location/Qualifiers

Modified-site 3

Modified-site /note= "optionally hydroxylated"

Modified-site 18

/note= "amidated"

US589340-A.

XX 31-DEC-1996.

XX 07-JUN-1995; 95US-00477383.

XX 23-JUN-1993; 93US-00084848.

XX 19-OCT-1993; 93US-00137800.

XX (UTAH) UNIV UTAH RES FOUND.

XX Santos AD, Hillyard DR, McIntosh JM, Olivera BM, Cruz LJ;

XX WPI; 1997-076840/07.

XX Identifying nucleic acid encoding A-lineage conotoxin peptide(s) by

XX amplification - uses primers corresponding to conserved regions in the

XX signal sequence and 3'-untranslated regions, useful e.g. in treatment of

XX small cell lung cancer.

XX Disclosure; Col 6; 36pp; English.

XX AAW12726-W12769 represent conotoxin peptides. This sequence represents

XX the A-lineage conotoxin U008 peptide isolated from *Conus ermineus*. These

XX sequences are identified using the method of the invention. The method of

XX the invention is for identifying DNA encoding A-lineage conotoxin

XX peptides by subjecting *Conus* nucleic acid to amplification with primer

XX sequences (see AAW59714 and AAW59715). The primers are specific for the

XX signal sequence and 3'-untranslated (3'UTR) regions of the conotoxin

XX gene, which are highly homologous between conotoxins, and are therefore

XX suitable sites for detection. A-lineage conotoxins include alpha-

XX conotoxins, and kappa-conotoxins. Alpha-conotoxins are powerful

XX inhibitors of synaptic transmission at the neuromuscular junction, and

XX are usually nicotinic acetylcholine receptor blockers. Kappa-conotoxins

XX act on the voltage sensitive sodium and potassium channels. The

XX conotoxins identified can be used as muscle relaxants, in the diagnosis

XX of myasthenia gravis, and for the treatment or diagnosis of small cell

XX lung cancer. For the treatment of small cell lung cancer, the conotoxin

XX peptides act by binding to the nicotinic receptors, and thereby blocking

XX the nicotine/cytosine stimulated release of the mitogen 5-

XX hydroxytryptamine. (Updated on 25-MAR-2003 to correct PF field.) (Updated

XX on 27-AUG-2003 to correct OS field.)

XX Sequence 18 AA;

Query Match 37.4%; Score 46; DB 2; Length 18;

Best Local Similarity 46.7%; Pred. No. 35;

Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 5 CCLIPACRRNHKKFC 19

Db 4 CCSNPACNVNPPQIC 18

RESULT 20

ABG99823

ID ABG99823 standard; peptide; 16 AA.

XX AC ABG99823;

XX 17-JAN-2003 (first entry)

XX Conus sp conotoxin-associated peptide SEQ ID 608.

Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator; ligand-gated ion channel modulator; pain-relief.

XX Conus magus.

XX WO200264740-A2.

XX 22-AUG-2002.

XX 11-FEB-2002; 2002WO-US003887.

09-FEB-2001; 2001US-0267408P.

(COGN-) COGNETIX INC.
(UTAH) UNIV UTAH RES FOUND.

Olivera BM, McIntosh JM, Watkins M, Garrett JF, Cruz LJ;
Grille M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;
WPI; 2002-706921/76.

New cone snail conotoxin peptides, useful as a pain reliever for
alleviating pain in an individual suffering from pain or who is about to
be subjected to a pain-causing event, or for treating voltage-gated ion
channel disorders.

Claim 1; Page 299; 305pp; English.

This invention describes novel conotoxin peptides from the cone snail,
genus *Conus* which have analgesic activity and can act as a voltage-gated
ion channel modulator or a ligand-gated ion channel modulator. The
conotoxin peptide is useful as a pain-relieving agent for alleviating
pain in an individual who is either exhibiting pain or is about to be
subjected to a pain-causing event. The conotoxin peptide is also useful
for treating or preventing disorders associated with voltage-gated ion
channel disorders, ligand-gated ion channel disorders or receptor
disorders. The radiolabeled conotoxin peptide is also useful for
characterizing a new site on these receptors or channels, and for
screening and identifying novel small molecules that interact with the
above-mentioned channels or receptors, which are monoamine transporters.
ABG9360-ABG99853 represent the conotoxin protein and peptides described
in the disclosure of the invention

Sequence 16 AA;

Query Match 36.6%; Score 45; DB 5; Length 16;
Best Local Similarity 40.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19
|||
2 CCVHPTCHLEHSLC 16

SULT 21
187520

AA87520 standard; peptide; 18 AA.

AA87520;

18-JUL-2000 (first entry)

Mature conotoxin peptide #1.

Mature conotoxin; brocade cone shell; line cone shell; drug screening;
neuronal inhibitor; muscle inhibitor.

Conus sp.

CN1237584-A.

08-DEC-1999.

30-APR-1999; 99CN-00106070.

30-APR-1999; 99CN-00106070.

(BIOL-) BIOLOGICAL ENG INST ACAD MILITARY MEDICI.

Lu B, Huang P;

WPI; 2000-351193/31.

PT Conotoxin peptide from brocade cone shells useful as analgesic.

XX Claim 1A; Page 2; 20pp; Chinese.

XX The invention relates to 14 novel mature conotoxin peptides from marine
snails (*Conus* species); conotoxin precursor proteins; and cDNAs encoding
the conotoxin precursors. The mature peptide sequences were discovered by
obtaining conotoxin cDNA sequences from mRNA from the brocade cone shell
(*Conus textile*) or the line cone shell (*Conus striatus*). The cDNA
sequences were used to determine the conotoxin precursor protein
sequences, and the sequences of the mature conotoxin peptides were
inferred from the precursor sequences. The mature conotoxin peptides can
be obtained via chemical synthesis or by in vitro gene expression.
Conotoxins inhibit the function of neurons and muscle cells. Certain
conotoxins interfere with synaptic transmission, while others act on
muscle or at the neuromuscular junction. The 14 novel conotoxins have
unique receptor specificity and affinity, so can be used as screening
tools to identify new drugs. Conotoxin #11 (AA87540) may be used for
pain relief. Sequences AA87420, AA87522, AA87524, AA87526, AA87528,
AA87530, AA87532, AA87534, AA87536, AA87538, AA87540, AA87542,
AA87544 and AA87546 represent mature conotoxins #1-#14, respectively
SQ Sequence 18 AA;

Query Match 36.6%; Score 45; DB 3; Length 18;
Best Local Similarity 40.0%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19
|||
Db 3 CCSDPRCNSHPELC 17

RESULT 22
AA875279

ID AAR75279 standard; peptide; 16 AA.

XX AAR75279;

XX 21-DEC-1995 (first entry)

DE A-lineage conotoxin MG-1 peptide.

XX Conotoxin; neuromuscular; synapse; signal transmission; inhibitor.

XX *Conus* magus.

XX Key Location/Qualifiers

FT Misc-difference 6 /label= Pro or OTHER

FT /note= "Hydroxyproline"

FT Modified-site 16

FT /note= "preferably amidated"

XX WO9511256-A1.

XX 27-APR-1995.

XX 19-OCT-1994; 94WO-US011927.

XX 19-OCT-1993; 93US-00137800.

XX (UTAH) UNIV UTAH RES FOUND.

XX Olivera BM, Cruz LJ, Hillyard DR, McIntosh JM, Santos AD;

XX WPI; 1995-170189/22.

XX New A-lineage conotoxin peptide(s) - which inhibit synaptic transmission
at the neuromuscular junction or are active against potassium or sodium
channels.

XX Claim 1; Page 43; 66pp; English.

The kappa-conotoxin, alpha conotoxin and alpha-like conotoxin peptides all belong to a group of peptides known as the A-lineage conotoxin peptides. The A-lineage conotoxin peptides have a wide variety of pharmacological uses. The A-lineage conotoxin peptides claimed (AA75264-R75293) are useful for the inhibition of synaptic transmission at neuromuscular junctions by blocking nicotinic acetylcholine receptors and they also have activity against voltage-gated Na and K channels

Sequence 16 AA;

Query Match 35.8%; Score 44; DB 2; Length 16;
 Best Local Similarity 40.0%; Pred. No. 57;
 Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

5 CCLIPACRHHKKFC 19
 |||||
 2 CCSNPVCHLEHSLC 16

RESULT 23
 AA24886
 AAW24886 standard; peptide; 16 AA.

AAW24886;

25-MAR-2003 (revised)
 15-OCT-1997 (first entry)

Predatory cone snail venom alpha-conotoxin MG-1.

Conotoxin; venom; predatory; cone snail; Conus; A-lineage; inhibitor;
 synaptic transmission; neuromuscular junction; block; alpha-conotoxin;
 nicotinic acetylcholine receptor; kappa-conotoxin;
 voltage-sensitive potassium CHANNEL; sodium channel.

Conus magus.

Key Location/Qualifiers
 Modified-site 16
 /note= "optionally 4Hyp"

US5633347-A.

27-MAY-1997.

07-JUN-1995; 95US-00480750.

29-JUN-1993; 93US-00084848.

19-OCT-1993; 93US-00137800.

(UTAH) UNIV UTAH RES FOUND.

Hillyard DR, Cruz LJ, McIntosh JM, Santos AO, Olivera BM;

WPI; 1997-309336/28.

New kappa-conotoxin peptide(s) - present in venom of fish-hunting cone snail.

Disclosure; Col 5; 37pp; English.

The peptides AAW24878-W24900 represent novel toxin peptides isolated from the venom of various predatory cone snails of the genus Conus. The peptides are A-lineage conotoxin peptides which fall into 3 groups dependent on their amino acid sequences: (i) alpha-3/5 have a core sequence CXXXXXXXXC where X is any amino acid; (ii) alpha-4/7 have a core sequence CXXXXXXXXC and (iii) kappa-7/2/1/3 have the core sequence CXXXXXXXCXCCXXC. The peptide presented here was isolated from Conus magus and falls into the alpha-4/7 category. Alpha-conotoxin peptides are potent inhibitors of synaptic transmission at the neuromuscular junction by blocking nicotinic acetylcholine receptors, whereas kappa-conotoxins have activities against voltage-sensitive

CC potassium or sodium channels. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 16 AA;

Query Match 35.8%; Score 44; DB 2; Length 16;
 Best Local Similarity 40.0%; Pred. No. 57;
 Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

5 CCLIPACRHHKKFC 19
 |||||
 2 CCSNPVCHLEHSLC 16

RESULT 24
 AA24899
 ID AAW24899 standard; peptide; 16 AA.

AAW24899;

25-MAR-2003 (revised)
 15-OCT-1997 (first entry)

Predatory cone snail venom alpha-conotoxin MII.

Conotoxin; venom; predatory; cone snail; Conus; A-lineage; inhibitor;
 synaptic transmission; neuromuscular junction; block; alpha-conotoxin;
 nicotinic acetylcholine receptor; kappa-conotoxin;
 voltage-sensitive potassium CHANNEL; sodium channel.

Conus magus.

Key Location/Qualifiers
 Modified-site 16
 /note= "amidated C-terminus"

US5633347-A.

27-MAY-1997.

07-JUN-1995; 95US-00480750.

29-JUN-1993; 93US-00084848.

19-OCT-1993; 93US-00137800.

(UTAH) UNIV UTAH RES FOUND.

Hillyard DR, Cruz LJ, McIntosh JM, Santos AO, Olivera BM;

WPI; 1997-309336/28.

New kappa-conotoxin peptide(s) - present in venom of fish-hunting cone snail.

Disclosure; Col 6; 37pp; English.

The peptides AAW24878-W24900 represent novel toxin peptides isolated from the venom of various predatory cone snails of the genus Conus. The peptides are A-lineage conotoxin peptides which fall into 3 groups dependent on their amino acid sequences: (i) alpha-3/5 have a core sequence CXXXXXXXXC where X is any amino acid; (ii) alpha-4/7 have a core sequence CXXXXXXXCXCCXXC; and (iii) kappa-7/2/1/3 have the core sequence CXXXXXXXCXCCXXC. The peptide presented here was isolated from Conus magus and falls into the alpha-4/7 category. Alpha-conotoxin peptides are potent inhibitors of synaptic transmission at the neuromuscular junction by blocking nicotinic acetylcholine receptors, whereas kappa-conotoxins have activities against voltage-sensitive potassium or sodium channels. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 16 AA;

Query Match 35.8%; Score 44; DB 2; Length 16;

Best Local Similarity 40.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

5 CCLIPACRRNKKFC 19
|||
2 CCNPNVCHLEHSLC 16

SULT 25
W12741

AAW12741 standard; peptide; 16 AA.

AAW12741;

25-MAR-2003 (revised)
16-APR-1997 (first entry)

A-lineage conotoxin peptide MG-1.

Polymerase chain reaction; PCR; primer; amplify; conotoxin; Conus;
inhibitor; synaptic transmission; neuromuscular junction; sodium channel;
nicotinic acetylcholine receptor; potassium channel; muscle relaxant;
myasthenia gravis; small cell lung cancer; therapy.

Conus magus.

Key Location/Qualifiers
Modified-site 6 /note= "optionally hydroxylated"
Modified-site 16 /note= "amidated"

US5589340-A.

31-DEC-1996.

07-JUN-1995; 95US-00477383.

29-JUN-1993; 93US-00084848.
19-OCT-1993; 93US-00137800.

(UTAH) UNIV UTAH RES FOUND.

Santos AD, Hillyard DR, McIntosh JM, Olivera BM, Cruz LJ;

WPI; 1997-076840/07.

Identifying nucleic acid encoding A-lineage conotoxin peptide(s) by
amplification - uses primers corresponding to conserved regions in the
signal sequence and 3'-untranslated regions, useful e.g. in treatment of
small cell lung cancer.

Disclosure; Col 5; 36pp; English.

AAW12726-W12769 represent conotoxin peptides. This sequence represents
the A-lineage conotoxin MG-1 peptide isolated from Conus magus. These
sequences are identified using the method of the invention. The method of
the invention is for identifying DNA encoding A-lineage conotoxin
peptides by subjecting Conus nucleic acid to amplification with primer
sequences (see AAT59714 and AAT59715). The primers are specific for the
signal sequence and 3'-untranslated (3'UTR) regions of the conotoxin
gene, which are highly homologous between conotoxins, and are therefore
suitable sites for detection. A-lineage conotoxins include alpha-
conotoxins, and kappa-conotoxins. Alpha-conotoxins are powerful
inhibitors of synaptic transmission at the neuromuscular junction, and
are usually nicotinic acetylcholine receptor blockers. Kappa-conotoxins
act on the voltage sensitive sodium and potassium channels. The
conotoxins identified can be used as muscle relaxants, in the diagnosis
of myasthenia gravis, and for the treatment or diagnosis of small cell
lung cancer. For the treatment of small cell lung cancer, the conotoxin
peptides act by binding to the nicotinic receptors, and thereby blocking
the nicotine/cytosine stimulated release of the mitogen 5-
hydroxytryptamine. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 16 AA;
SQ

Query Match 35.8%; Score 44; DB 2; Length 16;
Best Local Similarity 40.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 5 CCLIPACRRNKKFC 19
|||
Db 2 CCNPNVCHLEHSLC 16

RESULT 26

AAW12753

ID AAW12753 standard; peptide; 16 AA.

XX AAW12753;

XX 25-MAR-2003 (revised)

DT 16-APR-1997 (first entry)

XX A-lineage conotoxin peptide MII.

Polymerase chain reaction; PCR; primer; amplify; conotoxin; Conus;
inhibitor; synaptic transmission; neuromuscular junction; sodium channel;
nicotinic acetylcholine receptor; potassium channel; muscle relaxant;
myasthenia gravis; small cell lung cancer; therapy.

Conus magus.

Key Location/Qualifiers
FT Modified-site 16 /note= "amidated"

XX US5589340-A.

XX 31-DEC-1996.

XX 07-JUN-1995; 95US-00477383.

XX 29-JUN-1993; 93US-00084848.

XX 19-OCT-1993; 93US-00137800.

XX (UTAH) UNIV UTAH RES FOUND.

XX Santos AD, Hillyard DR, McIntosh JM, Olivera BM, Cruz LJ;

XX WPI; 1997-076840/07.

XX Identifying nucleic acid encoding A-lineage conotoxin peptide(s) by
amplification - uses primers corresponding to conserved regions in the
signal sequence and 3'-untranslated regions, useful e.g. in treatment of
small cell lung cancer.

XX Disclosure; Col 6; 36pp; English.

AAW12726-W12769 represent conotoxin peptides. This sequence represents
the A-lineage conotoxin MII peptide isolated from Conus magus. These
sequences are identified using the method of the invention. The method of
the invention is for identifying DNA encoding A-lineage conotoxin
peptides by subjecting Conus nucleic acid to amplification with primer
sequences (see AAT59714 and AAT59715). The primers are specific for the
signal sequence and 3'-untranslated (3'UTR) regions of the conotoxin
gene, which are highly homologous between conotoxins, and are therefore
suitable sites for detection. A-lineage conotoxins include alpha-
conotoxins, and kappa-conotoxins. Alpha-conotoxins are powerful
inhibitors of synaptic transmission at the neuromuscular junction, and
are usually nicotinic acetylcholine receptor blockers. Kappa-conotoxins
act on the voltage sensitive sodium and potassium channels. The
conotoxins identified can be used as muscle relaxants, in the diagnosis
of myasthenia gravis, and for the treatment or diagnosis of small cell
lung cancer. For the treatment of small cell lung cancer, the conotoxin
peptides act by binding to the nicotinic receptors, and thereby blocking
the nicotine/cytosine stimulated release of the mitogen 5-
hydroxytryptamine. (Updated on 25-MAR-2003 to correct PF field.)

the nicotine/cytosine stimulated release of the mitogen 5-hydroxytryptamine. (Updated on 25-MAR-2003 to correct PF field.)

Sequence 16 AA;

Query Match 35.8%; Score 44; DB 2; Length 16;
Best Local Similarity 40.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19

2 CCSNPVCHLEHSNLC 16

RESULT 27

W57903

AAW57903 standard; peptide; 16 AA.

AAW57903;

25-SEP-1998 (first entry)

Conotoxin peptide MII.

Conotoxin peptide; ImI; MII; cardiovascular agent; altered heart rate;
altered blood pressure; nicotinic acetylcholine receptor antagonist;
B neuron blocker; venom; marine snail; C neuron blocker;
sympathetic impulse.

Conus imperialis.

Key Location/Qualifiers

Disulfide-bond 2..8

Disulfide-bond 3..16

WO9822126-A1.

28-MAY-1998.

17-NOV-1997; 97WO-US020669.

18-NOV-1996; 96US-0031141P.

(UTAH) UNIV UTAH RES FOUND.

McIntosh JM, Olivera BM, Yoshikami D;

WPI; 1998-322346/28.

Use of the conotoxin peptide(s) ImI and MII - as agents which can regulate heart rate or blood pressure.

Claim 1; Page 4; 24pp; English.

This sequence represents the conotoxin peptide ImI. This sequence and the MII conotoxin peptide (see AAW57903) can be used in the method of the invention for the treatment of a patient who has an altered heart rate or an altered blood pressure. The peptides are found in the venom of marine snails of the genus Conus. They are active as nicotinic acetylcholine receptor antagonists. They differentially block the B and C neurones, and are thus able to differentially block sympathetic impulses to the heart affecting the heart rate and blood pressure. The above agents are capable of discretely affecting the heart rate or blood pressure, without affecting other muscles

Sequence 16 AA;

Query Match 35.8%; Score 44; DB 2; Length 16;
Best Local Similarity 40.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19

||| | | | |

Db 2 CCSNPVCHLEHSNLC 16

RESULT 28

AAI24167

ID AAY24167 standard; peptide; 16 AA.

XX AC AAY24167;

XX 10-SEP-1999 (first entry)

XX Alpha-conotoxin peptide SEQ ID NO:2.

XX Alpha-conotoxin; neuronal nicotinic acetylcholine receptor; nAChR;

small cell lung carcinoma; cardiovascular disorder; nicotine addiction;

gastric motility disorder; urinary incontinence; mood disorder;

bipolar disorder; unipolar depression; dysthymia;

seasonal effective disorder.

XX Conus magus.

XX WO9933482-A1.

XX 08-JUL-1999.

XX 23-DEC-1998; 98WO-US027367.

XX 31-DEC-1997; 97US-0070153P.

PR 03-APR-1998; 98US-0080588P.

XX (UTAH) UNIV UTAH RES FOUND.

XX Olivera BM, McIntosh JM, Yoshikami D, Cartier GE, Luo S;

XX WPI; 1999-405367/34.

XX Alpha-conotoxin peptides that are used to treat disorders regulated at neuronal nicotinic acetylcholine receptors.

XX Disclosure; Page 6; 40pp; English.

XX The present sequence represents an example of an alpha-conotoxin peptide, which can be used to treat disorders regulated at neuronal nicotinic acetylcholine receptors (nAChR). The alpha-conotoxins are useful for preparing a pharmaceutical composition for treating disorders regulated at neuronal nAChR, especially alpha 3 beta 2, alpha 3 beta 4 or alpha 7-containing nAChR. Disorders that can be treated include cardiovascular disorders, a gastric motility disorder, urinary incontinence, nicotine addiction, a mood disorder or small cell lung carcinoma. Mood disorders include bipolar disorder, unipolar depression, dysthymia and seasonal effective disorder. The alpha-conotoxins can also be used for diagnosis of small cell lung carcinoma. The alpha-conotoxin antagonists are able to discriminate between non-symmetrical ligand binding interfaces present on the nAChR. The alpha-conotoxin has the ability to potentially block any receptor containing an alpha beta subunit interface, regardless of what other subunits may be present in the receptor complex

XX Sequence 16 AA;

Query Match 35.8%; Score 44; DB 2; Length 16;

Best Local Similarity 40.0%; Pred. No. 57;

Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19

||| | | | |

Db 2 CCSNPVCHLEHSNLC 16

RESULT 29

AAI09520

ID AAY09520 standard; peptide; 16 AA.

XX AC AAY09520;

1 Key Location/Qualifiers
 16 Modified-site /note= "C-terminal amide"

WO200279236-A1.

10-OCT-2002.

28-MAR-2002; 2002WO-AUG00411.

29-MAR-2001; 2001AU-00004094.

(LIVE/) LIVETT B.

(KHALI/) KHALIL Z.

(GAYL/) GAYLER K.

(DOWN/) DOWN J.

Livett B, Khalil Z, Gayler K, Down J;

WPI; 2003-103260/09.

New alpha- conotoxin-like peptides that inhibit the activity of neuronal nicotinic acetylcholine receptor, useful for treating stroke, pain, schizophrenia, Parkinson's disease, small cell lung carcinoma or Alzheimer's disease.

Claim 8; Page 57; 87pp; English.

The invention relates to an isolated alpha-conotoxin-like peptide sequence. The activity of peptides of the invention may be described as cerebroprotective, analgesic, anticonvulsant, neuroleptic, antiparkinsonian, cytostatic, nontropic and neuroprotective. Peptides of the invention are neuronal nicotinic acetylcholine receptor (nAChR) inhibitors. The alpha-conotoxin-like peptide is useful for treating a condition mediated by a neuronal nicotinic acetylcholine receptor, e.g. stroke, pain (e.g. cancer related pain, post-surgical pain, oral or dental pain, referred trigeminal neuralgia, post-herpetic neuralgia, phantom limb pain, fibromyalgia, reflex sympathetic dystrophy, pain associated with inflammatory conditions, rheumatoid arthritis or inflammatory arthritis, or pain resulting from conditions associated with neurogenic or neuropathic pain), epilepsy, nicotine addiction, schizophrenia, Parkinson's disease, small cell lung carcinoma, or Alzheimer's disease. The alpha-conotoxin-like peptide is also useful for accelerating recovery from nerve injury. The peptides are also useful as research reagents for investigating nicotinic acetylcholine receptor physiology and pharmacology. The current sequence represents an alpha-conotoxin peptide of the invention that has been designated vcl.1

Sequence 16 AA;

Query Match 35.8%; Score 44; DB 6; Length 16;
 Best Local Similarity 40.0%; Pred. No. 57;
 Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Y 5 CCLIPACRRNHKKFC 19

b 2 CCSDPRCNYDHPIC 16

RESULT 32

AY24156

D AAY24156 standard; peptide; 17 AA.

X C AAY24156;

X T 10-SEP-1999 (first entry)

X E Alpha-conotoxin peptide SEQ ID NO:3.

X W Alpha-conotoxin; neuronal nicotinic acetylcholine receptor; nAChR;
 W small cell lung carcinoma; cardiovascular disorder; nicotine addiction;
 W gastric motility disorder; urinary incontinence; mood disorder;
 W bipolar disorder; unipolar depression; dysthymia;

KW seasonal effective disorder.

OS Conus magus.

OS Synthetic.

XX WO9933482-A1.

XX 08-JUL-1999.

XX 23-DEC-1998; 98WO-US027367.

XX 31-DEC-1997; 97US-0070153P.

PR 03-APR-1998; 98US-0080588P.

XX (UTAH) UNIV UTAH RES FOUND.

XX Olivera BM, McIntosh JM, Yoshikami D, Cartier GE, Luo S;

XX WPI; 1999-405367/34.

XX Alpha-conotoxin peptides that are used to treat disorders regulated at neuronal nicotinic acetylcholine receptors.

XX Claim 12; Page 27; 40pp; English.

CC The present sequence represents a specifically claimed example of an alpha-conotoxin from the general formula given in AAY24155, which can be used to treat disorders regulated at neuronal nicotinic acetylcholine receptors (nAChR). The alpha-conotoxins are useful for preparing a pharmaceutical composition for treating disorders regulated at neuronal nAChR, especially alpha 3 beta 2, alpha 3 beta 4 or alpha 7-containing nAChR. Disorders that can be treated include cardiovascular disorders, a gastric motility disorder, urinary incontinence, nicotine addiction, a mood disorder or small cell lung carcinoma. Mood disorders include bipolar disorder, unipolar depression, dysthymia and seasonal affective disorder. The alpha-conotoxins can also be used for diagnosis of small cell lung carcinoma. The alpha-conotoxin antagonists are able to discriminate between non-symmetrical ligand binding interfaces present on the nAChR. The alpha-conotoxin has the ability to potentially block any CC receptor containing an alpha beta subunit interface, regardless of what other subunits may be present in the receptor complex

XX Sequence 17 AA;

Query Match 35.8%; Score 44; DB 2; Length 17;
 Best Local Similarity 40.0%; Pred. No. 60;
 Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19

Db 3 CCSPVCHLEHSLC 17

RESULT 33

ABG99818

ID ABG99818 standard; peptide; 17 AA.

XX AC ABG99818;

XX 17-JAN-2003 (first entry)

DE Conus sp conotoxin-associated peptide SEQ ID 603.

XX Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;
 KW ligand-gated ion channel modulator; pain-relief.

XX Conus omaria.

OS WO200264740-A2.

PN 22-AUG-2002.

XX 11-FEB-2002; 2002WO-US003887.

PF

This invention describes novel conotoxin peptides from the cone snail, genus *Conus* which have analgesic activity and can act as a voltage-gated ion channel modulator or a ligand-gated ion channel modulator. The conotoxin peptide is useful as a pain-relieving agent for alleviating pain in an individual who is either exhibiting pain or is about to be subjected to a pain-causing event. The conotoxin peptide is also useful for treating or preventing disorders associated with voltage-gated ion channel disorders, ligand-gated ion channel disorders or receptor disorders. The radiolabeled conotoxin peptide is also useful for characterizing a new site on these receptors or channels, and for screening and identifying novel small molecules that interact with the above-mentioned channels or receptors, which are monoamine transporters. ABG9360-ABG99853 represent the conotoxin protein and peptides described in the disclosure of the invention

Sequence 17 AA;

Query Match	35.8%	Score 44;	DB 5;	Length 17;
Best Local Similarity	46.7%	Pred. NO. 60;		
Matches	7;	Conservative	1;	Mismatches 7; Indels 0; Gaps 0;
	5	CCILPACRRNHKKFC	19	
	2	CCSHPCVNVNPHIC	16	

Search completed: February 18, 2004, 06:27:31
 > time : 53 secs

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protein - protein search, using sw model

on: February 18, 2004, 06:28:55 ; Search time 34 Seconds

(without alignments)
117.997 Million cell updates/sec

le: US-09-806-376-1

fact score: 123

nence: 1 FNMRCCLIPACRRNHKKFC 19

ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 809742 seqs, 211153259 residues

al number of hits satisfying chosen parameters: 181359

imum DB seq length: 0

imum DB seq length: 19

it-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

abase : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	Query Match	Length	DB ID	Description
1	49	39.8	17	14	US-10-072-602B-605
2	48	39.0	16	9	US-09-897-465-9
3	47	38.2	16	9	US-09-897-465-10
4	45	36.6	16	14	US-10-072-602B-608
5	44	35.8	16	9	US-09-897-465-2
6	44	35.8	16	14	US-10-072-602B-612
7	44	35.8	17	9	US-09-897-465-3
8	44	35.8	17	14	US-10-072-602B-602
9	44	35.8	17	14	US-10-072-602B-603
10	44	35.8	17	14	US-10-072-602B-610
11	44	35.8	17	14	US-10-072-602B-618
12	43	35.0	16	9	US-09-897-465-11
13	43	35.0	19	10	US-09-910-009A-421
14	42	34.1	16	9	US-09-897-465-4
15	42	34.1	16	9	US-09-897-465-12

Sequence 606, App
Sequence 613, App
Sequence 440, App
Sequence 21, Appl
Sequence 607, App
Sequence 5, Appl
Sequence 6, Appl
Sequence 410, App
Sequence 604, App
Sequence 113, App
Sequence 615, App
Sequence 8, Appl
Sequence 34, Appl
Sequence 609, App
Sequence 346, App
Sequence 170, App
Sequence 171, App
Sequence 172, App
Sequence 442, App
Sequence 429, App
Sequence 58, Appl
Sequence 166, App
Sequence 621, App
Sequence 11, Appl
Sequence 417, App
Sequence 403, App
Sequence 404, App
Sequence 150, App
Sequence 398, App
Sequence 105, App
Sequence 102, App
Sequence 108, App
Sequence 112, App
Sequence 159, App
Sequence 170, App

ALIGNMENTS

RESULT 1
US-10-072-602B-605
Sequence 605, Application US/10072602B
Publication No. US20030109670A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J, Michael
APPLICANT: Watkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Grilley, Michelle
APPLICANT: Schoenfeld, Robert M.
APPLICANT: Walker, Craig
APPLICANT: Shetty, Reshma
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Cone Snail Peptides
FILE REFERENCE: 2314-249
CURRENT APPLICATION NUMBER: US/10/072,602B
CURRENT FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/267,408
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 638
SOFTWARE: Patent in version 3.0
SEQ ID NO 605
LENGTH: 17
TYPE: PRT
ORGANISM: Conus bandanus
US-10-072-602B-605

Query Match 39.8%; Score 49; DB 14; Length 17;
Best Local Similarity 46.7%; Pred. No. 5.5;

Matches 7; Conservative 2; Mismatches 6; Indels 6; Gaps 0;
Query Match 38.2%; Score 47; DB 9; Length 16;
Best Local Similarity 40.0%; Pred. No. 9.7;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19
|||:|:|:|

3 CCTHPACHVSHPELC 17
|||:|:|:|

SULT 2

-09-897-465-9

Sequence 9, Application US/09897465

Patent No. US20020022715A1

GENERAL INFORMATION:

APPLICANT: Olivera, Baldomero M.

APPLICANT: McIntosh, J. Michael

APPLICANT: Yoshikami, Doju

APPLICANT: Cartier, G. Edward

APPLICANT: Luo, Siqin

TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides

FILE REFERENCE: Uses of Alpha-Conotoxins

CURRENT APPLICATION NUMBER: US/09/897,465

CURRENT FILING DATE: 2001-07-03

PRIOR APPLICATION NUMBER: US 60/080,588

PRIOR FILING DATE: 1998-04-03

PRIOR APPLICATION NUMBER: US 60/070,153

PRIOR FILING DATE: 1997-12-31

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 9

LENGTH: 16

TYPE: PRT

ORGANISM: Conus purpurascens

-09-897-465-9

Query Match 39.0%; Score 48; DB 9; Length 16;
Best Local Similarity 40.0%; Pred. No. 7.1;
Matches 6; Conservative 3; Mismatches 6; Indels 6; Gaps 0;

5 CCLIPACRRNHKKFC 19
|||:|:|:|

2 CCSLPPCANNDYC 16
|||:|:|:|

SULT 3

-09-897-465-10

Sequence 10, Application US/09897465

Patent No. US20020022715A1

GENERAL INFORMATION:

APPLICANT: Olivera, Baldomero M.

APPLICANT: McIntosh, J. Michael

APPLICANT: Yoshikami, Doju

APPLICANT: Cartier, G. Edward

APPLICANT: Luo, Siqin

TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides

FILE REFERENCE: Uses of Alpha-Conotoxins

CURRENT APPLICATION NUMBER: US/09/897,465

CURRENT FILING DATE: 2001-07-03

PRIOR APPLICATION NUMBER: US 60/080,588

PRIOR FILING DATE: 1998-04-03

PRIOR APPLICATION NUMBER: US 60/070,153

PRIOR FILING DATE: 1997-12-31

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 10

LENGTH: 16

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: A10L derivative

OTHER INFORMATION: of C. purpurascens PnIA

-09-897-465-10

Query Match 38.2%; Score 47; DB 9; Length 16;
Best Local Similarity 40.0%; Pred. No. 9.7;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19
|||:|:|:|

2 CCSLPPCANNDYC 16
|||:|:|:|

RESULT 4

US-10-072-602B-608

Sequence 608, Application US/10072602B

Publication No. US20030109670A1

GENERAL INFORMATION:

APPLICANT: University of Utah Research Foundation

APPLICANT: Cognetix, Inc.

APPLICANT: Olivera, Baldomero M.

APPLICANT: McIntosh, J. Michael

APPLICANT: Watkins, James B.

APPLICANT: Garrett, Maren E.

APPLICANT: Cruz, Lourdes J.

APPLICANT: Grilley, Michelle

APPLICANT: Schoenfeld, Robert M.

APPLICANT: Walker, Craig

APPLICANT: Shetty, Reshma

APPLICANT: Jones, Robert M.

TITLE OF INVENTION: Cone Snail Peptides

FILE REFERENCE: 2314-249

CURRENT APPLICATION NUMBER: US/10/072,602B

CURRENT FILING DATE: 2002-02-11

PRIOR APPLICATION NUMBER: US 60/267,408

PRIOR FILING DATE: 2001-02-09

NUMBER OF SEQ ID NOS: 638

SOFTWARE: PatentIn version 3.0

SEQ ID NO 608

LENGTH: 16

TYPE: PRT

ORGANISM: Conus magus

US-10-072-602B-608

Query Match 36.6%; Score 45; DB 14; Length 16;
Best Local Similarity 40.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19
|||:|:|:|

2 CCYHPTCHLEHSLC 16
|||:|:|:|

RESULT 5

US-09-897-465-2

Sequence 2, Application US/09897465

Patent No. US20020022715A1

GENERAL INFORMATION:

APPLICANT: Olivera, Baldomero M.

APPLICANT: McIntosh, J. Michael

APPLICANT: Yoshikami, Doju

APPLICANT: Cartier, G. Edward

APPLICANT: Luo, Siqin

TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides

FILE REFERENCE: Uses of Alpha-Conotoxins

CURRENT APPLICATION NUMBER: US/09/897,465

CURRENT FILING DATE: 2001-07-03

PRIOR APPLICATION NUMBER: US 60/080,588

PRIOR FILING DATE: 1998-04-03

PRIOR APPLICATION NUMBER: US 60/070,153

PRIOR FILING DATE: 1997-12-31

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 16

TYPE: PRT

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ORGANISM: Conus magus
09-897-465-2
Query Match 35.8%; Score 44; DB 9; Length 16;
Best Local Similarity 40.0%; Pred. No. 24; 9; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19
||| ||| |||
2 CCSNPVCHLEHSNLC 16

UT 6
10-072-602B-612
Sequence 612, Application US/10072602B
Publication No. US20030109670A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Watkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Grilley, Michelle
APPLICANT: Schoenfeld, Robert M.
APPLICANT: Walker, Craig
APPLICANT: Jones, Reshma
APPLICANT: Shetty, Robert M.
TITLE OF INVENTION: Cone Snail Peptides
CURRENT APPLICATION NUMBER: US/10/072,602B
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/267,408
NUMBER OF SEQ ID NOS: 638
SOFTWARE: Patent in version 3.0
SEQ ID NO 612
LENGTH: 16
TYPE: PRT
ORGANISM: Conus leopardus
10-072-602B-612
Query Match 35.8%; Score 44; DB 14; Length 16;
Best Local Similarity 46.7%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19
||| ||| |||
1 CCSNPACRNYPNPAIC 15

BULT 7
09-897-465-3
Sequence 3, Application US/09897465
Patent No. US20020022715A1
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Yoshikami, Do'u
APPLICANT: Cartier, G. Edward
APPLICANT: Luo, Siqin
APPLICANT: University of Utah Research Foundation
TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
FILE REFERENCE: Uses of Alpha-Conotoxins
CURRENT APPLICATION NUMBER: US/09/897,465
CURRENT FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: US 60/080,588
PRIOR FILING DATE: 1998-04-03
PRIOR APPLICATION NUMBER: US 60/070,153
PRIOR FILING DATE: 1997-12-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patent in Ver. 2.0

; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Tyr derivative
; OTHER INFORMATION: of C. magus MI1
US-09-897-465-3
Query Match 35.8%; Score 44; DB 9; Length 17;
Best Local Similarity 40.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19
||| ||| |||
DB 3 CCSNPVCHLEHSNLC 17

RESULT 8
US-10-072-602B-602
Sequence 602, Application US/10072602B
Publication No. US20030109670A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Watkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Grilley, Michelle
APPLICANT: Schoenfeld, Robert M.
APPLICANT: Walker, Craig
APPLICANT: Shetty, Reshma
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Cone Snail Peptides
FILE REFERENCE: 2314-249
CURRENT APPLICATION NUMBER: US/10/072,602B
CURRENT FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/267,408
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 638
SOFTWARE: Patent in version 3.0
SEQ ID NO 602
LENGTH: 17
TYPE: PRT
ORGANISM: Conus omaria
US-10-072-602B-602
Query Match 35.8%; Score 44; DB 14; Length 17;
Best Local Similarity 46.7%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19
||| ||| |||
DB 2 CCSHPACNVNPNPIC 16

RESULT 9
US-10-072-602B-603
Sequence 603, Application US/10072602B
Publication No. US20030109670A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Watkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Grilley, Michelle
APPLICANT: Schoenfeld, Robert M.
APPLICANT: Walker, Craig
```

SULT 11
-10-072-602B-618
Sequence 618, Application US/10072602B
Publication No. US20030109670A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.

RESULT 13
US-09-910-009A-421

Sequence 421, Application US/09910009A
Publication No. US20030050234A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Garrett, James E.
APPLICANT: Watkins, Maren
APPLICANT: Cruz, Lourdes J.
APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
APPLICANT: Cartier, G. Edward
APPLICANT: Shen, Greg S.
APPLICANT: Wagstaff, John D.
TITLE OF INVENTION: Mu-Conopeptides
FILE REFERENCE: 2314-242
CURRENT APPLICATION NUMBER: US/09/910,009A
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,619
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/245,157
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/264,319
PRIOR FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: US 60/277,270
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 520
SOFTWARE: PatentIn version 3.0
SEQ ID NO 421
LENGTH: 19
TYPE: PRT
ORGANISM: Conus marmoreus
-09-910-009A-421

Query Match 35.0%; Score 43; DB 10; Length 19;
Best Local Similarity 66.7%; Pred. No. 38;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

4 RCLIPACR 12
: : : : :
3 QCCHLPACR 11

SULT 14
-09-897-465-4
Sequence 4, Application US/09897465
Patent No. US20020022715A1
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Yoshikami, Doju
APPLICANT: Cartier, G. Edward
APPLICANT: Luo, Siqin
APPLICANT: University of Utah Research Foundation
TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
FILE REFERENCE: Uses of Alpha-Conotoxins
CURRENT APPLICATION NUMBER: US/09/897,465
CURRENT FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: US 60/080,588
PRIOR FILING DATE: 1998-04-03
PRIOR APPLICATION NUMBER: US 60/070,153
PRIOR FILING DATE: 1997-12-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: FAT derivative
OTHER INFORMATION: of C. magus MII

US-09-897-465-4

Query Match 34.1%; Score 42; DB 9; Length 16;
Best Local Similarity 40.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19
: : : : :
DB 2 CCSNPVCFATHSNLC 16

RESULT 15
US-09-897-465-12
Sequence 12, Application US/09897465
Patent No. US20020022715A1
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Yoshikami, Doju
APPLICANT: Cartier, G. Edward
APPLICANT: Luo, Siqin
APPLICANT: University of Utah Research Foundation
TITLE OF INVENTION: Uses of Alpha-Conotoxins
FILE REFERENCE: Uses of Alpha-Conotoxins
CURRENT APPLICATION NUMBER: US/09/897,465
CURRENT FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: US 60/080,588
PRIOR FILING DATE: 1998-04-03
PRIOR APPLICATION NUMBER: US 60/070,153
PRIOR FILING DATE: 1997-12-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 16
TYPE: PRT
ORGANISM: Conus purpurascens
US-09-897-465-12

Query Match 34.1%; Score 42; DB 9; Length 16;
Best Local Similarity 33.3%; Pred. No. 45;
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19
: : : : :
DB 2 CCSLPPCALSNPDYC 16

RESULT 16
US-10-072-602B-606
Sequence 606, Application US/10072602B
Publication No. US20030109670A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Watkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Grilley, Michelle
APPLICANT: Schoenfeld, Robert M.
APPLICANT: Walker, Craig
APPLICANT: Shetty, Reshma
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Cone Snail Peptides
FILE REFERENCE: 2314-249
CURRENT APPLICATION NUMBER: US/10/072,602B
CURRENT FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/267,408
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 638
SOFTWARE: PatentIn version 3.0
SEQ ID NO 606


```
LENGTH: 17
TYPE: PRT
ORGANISM: Conus marmoreus
-10-072-602B-606

Query Match      34.1%; Score 42; DB 14; Length 17;
Best Local Similarity 40.0%; Pred. No. 47;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19
||| ||| : : :
3 CCTHPACHVSNPGLC 17

SULT 17
-10-072-602B-613
Sequence 613, Application US/10072602B
Publication No. US20030109670A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Watkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Grille, Michelle
APPLICANT: Schoenfeld, Robert M.
APPLICANT: Walker, Craig
APPLICANT: Shetty, Reshma
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Cone Snail Peptides
FILE REFERENCE: 2314-249
CURRENT APPLICATION NUMBER: US/10/072,602B
CURRENT FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/267,408
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 638
SOFTWARE: PatentIn version 3.0
SEQ ID NO 613
LENGTH: 17
TYPE: PRT
ORGANISM: Conus emaciatu
-10-072-602B-613

Query Match      33.3%; Score 41; DB 14; Length 17;
Best Local Similarity 40.0%; Pred. No. 64;
Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19
||| ||| : : :
2 CCNFPACASNPGLC 16

SULT 18
-09-910-009A-440
Sequence 440, Application US/09910009A
Publication No. US2003050234A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Garrett, James E.
APPLICANT: Watkins, Maren
APPLICANT: Cruz, Lourdes J.
APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
APPLICANT: Cartier, G. Edward
APPLICANT: Shen, Greg S.
APPLICANT: Wagstaff, John D.
TITLE OF INVENTION: Mu-Conopeptides
```

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FILE REFERENCE: 2314-242
CURRENT APPLICATION NUMBER: US/09/910,009A
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,619
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/245,157
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/264,319
PRIOR FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: US 60/277,270
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 520
SOFTWARE: PatentIn version 3.0
SEQ ID NO 440
LENGTH: 16
TYPE: PRT
ORGANISM: Conus marmoreus
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(16)
OTHER INFORMATION: Xaa is Hyp
US-09-910-009A-440

Query Match      31.7%; Score 39; DB 10; Length 16;
Best Local Similarity 71.4%; Pred. No. 11e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      5 CCLIPAC 11
DB      2 CCXLPAC 8
||| |||

RESULT 19
US-09-825-517A-21
Sequence 21, Application US/09825517A
Publication No. US20030203415A1
GENERAL INFORMATION:
APPLICANT: Rondon, Isaac J
APPLICANT: Ladner, Robert C
TITLE OF INVENTION: BINDING PEPTIDES FOR CARCINOEMBRYONIC
FILE REFERENCE: DYX-016.1 (3421.1005-001)
CURRENT APPLICATION NUMBER: US/09/825,517A
CURRENT FILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: US 09/541,345
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 151
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Isolate of TN10/9 library found not to bind CEA
US-09-825-517A-21

Query Match      31.7%; Score 39; DB 11; Length 16;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 NWRCCCLIP 9
DB      1 NWRCKLFP 8
||| |||

RESULT 20
US-10-072-602B-607
Sequence 607, Application US/10072602B
Publication No. US20030109670A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
```

APPLICANT: McIntosh, J. Michael
APPLICANT: Watkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Grilley, Michelle
APPLICANT: Schoenfeld, Robert M.
APPLICANT: Walker, Craig
APPLICANT: Shetty, Reehma
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Cone Snail Peptides
FILE REFERENCE: 2314-249
CURRENT APPLICATION NUMBER: US/10/072,602B
CURRENT FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/267,408
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 638
SOFTWARE: PatentIn version 3.0
SEQ ID NO 607
LENGTH: 15
TYPE: PRT
ORGANISM: Conus miles
-10-072-602B-607

Query Match 30.9%; Score 38; DB 14; Length 15;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
5 CCLIPACRRNHKKFC 19
||| :
1 CCNHPACAGKNSDLC 15

SULT 21

-09-897-465-5
Sequence 5, Application US/09897465
Patent No. US20020022715A1
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Yoshikami, Doju
APPLICANT: Cartier, G. Edward
APPLICANT: Luo, Sigin
APPLICANT: University of Utah Research Foundation
TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
FILE REFERENCE: Uses of Alpha-Conotoxins
CURRENT APPLICATION NUMBER: US/09/897,465
CURRENT FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: US 60/080,588
PRIOR FILING DATE: 1998-04-03
PRIOR APPLICATION NUMBER: US 60/070,153
PRIOR FILING DATE: 1997-12-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 16
TYPE: PRT
ORGANISM: Conus aulicus
-09-897-465-5

Query Match 30.9%; Score 38; DB 9; Length 16;
Best Local Similarity 33.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
5 CCLIPACRRNHKKFC 19
||| :
2 CCSYPPCFATNSDYC 16

SULT 22

-09-897-465-6
Sequence 6, Application US/09897465
Patent No. US20020022715A1
GENERAL INFORMATION:

APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Yoshikami, Doju
APPLICANT: Cartier, G. Edward
APPLICANT: Luo, Sigin
APPLICANT: University of Utah Research Foundation
TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
FILE REFERENCE: Uses of Alpha-Conotoxins
CURRENT APPLICATION NUMBER: US/09/897,465
CURRENT FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: US 60/080,588
PRIOR FILING DATE: 1998-04-03
PRIOR APPLICATION NUMBER: US 60/070,153
PRIOR FILING DATE: 1997-12-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Tyr derivative
US-09-897-465-6

Query Match 30.9%; Score 38; DB 9; Length 17;
Best Local Similarity 33.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19
||| :
Db 3 CCSYPPCFATNSDYC 17

RESULT 23

US-10-072-602B-410
Sequence 410, Application US/10072602B
Publication No. US20030109670A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Watkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Grilley, Michelle
APPLICANT: Schoenfeld, Robert M.
APPLICANT: Walker, Craig
APPLICANT: Shetty, Reehma
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Cone Snail Peptides
FILE REFERENCE: 2314-249
CURRENT APPLICATION NUMBER: US/10/072,602B
CURRENT FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/267,408
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 638
SOFTWARE: PatentIn version 3.0
SEQ ID NO 410
LENGTH: 17
TYPE: PRT
ORGANISM: Conus bandanus
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)...(17)
OTHER INFORMATION: Xaa at residues 2 and 15 is Glu or gamma-carboxy-Glu; Xaa at residues 1, 7 and 14 is Pro or hydroxy-Pro
US-10-072-602B-410

Query Match 30.9%; Score 38; DB 14; Length 17;
Best Local Similarity 40.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

5 CCLIPACRRNHKFC 19
3 CCTHXACHVSHXLC 17

SULT 24
-10-072-602B-604
Sequence 604, Application US/10072602B
Publication No. US20030109670A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Watkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Grilley, Michelle
APPLICANT: Schoenfeld, Robert M.
APPLICANT: Walker, Craig
APPLICANT: Shetty, Reshma
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Cone Snail Peptides
FILE REFERENCE: 2314-249
CURRENT APPLICATION NUMBER: US/10/072,602B
CURRENT FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/267,408
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 638
SOFTWARE: PatentIn version 3.0
SEQ ID NO 604
LENGTH: 19
TYPE: PRT
ORGANISM: Conus quercinus
-10-072-602B-604
Query Match 30.9%; Score 38; DB 14; Length 19;
Best Local Similarity 40.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
5 CCLIPACRRNHKFC 19
3 CCSDPACAVSNPDIC 17
SULT 25
-09-908-741-113
Sequence 113, Application US/09908741
Publication No. US20030050435A1
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Laver, Richard T.
APPLICANT: Watkins, Maren
APPLICANT: Hillyard, David R.
APPLICANT: McIntosh, J. Michael
APPLICANT: Schoenfeld, Robert M.
APPLICANT: Jones, Robert M.
APPLICANT: Nielsen, Jake
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Alpha Conotoxin Peptides
FILE REFERENCE: Alpha CIP
CURRENT APPLICATION NUMBER: US/09/908,741
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/116,881
PRIOR FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: US 60/116,882
PRIOR FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: US 09/488,799
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 60/219,407
PRIOR FILING DATE: 2000-07-20

PRIOR APPLICATION NUMBER: US 60/221,557
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PatentIn ver. 2.0
SEQ ID NO 113
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: MI Analog
US-09-908-741-113
Query Match 30.5%; Score 37.5; DB 10; Length 14;
Best Local Similarity 61.5%; Pred. No. 1.6e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
QY 4 RCLIPACRRNHK 16
DB 2 RCC-HPACQNTK 13
RESULT 26
US-10-072-602B-615
Sequence 615, Application US/10072602B
Publication No. US20030109670A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Watkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Grilley, Michelle
APPLICANT: Schoenfeld, Robert M.
APPLICANT: Walker, Craig
APPLICANT: Shetty, Reshma
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Cone Snail Peptides
FILE REFERENCE: 2314-249
CURRENT APPLICATION NUMBER: US/10/072,602B
CURRENT FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/267,408
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 638
SOFTWARE: PatentIn version 3.0
SEQ ID NO 615
LENGTH: 17
TYPE: PRT
ORGANISM: Conus cinereus gubba
US-10-072-602B-615
Query Match 30.5%; Score 37.5; DB 14; Length 17;
Best Local Similarity 46.7%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 6; Indels 1; Gaps 1;
QY 5 CCLIPACRRNHKFC 19
DB 3 CCSFPFCIANN-PFC 16
RESULT 27
US-09-897-465-8
Sequence 8, Application US/09897465
Patent No. US2002002715A1
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Yoshikami, Doju
APPLICANT: Cartier, G. Edward
APPLICANT: Luo, Siqin
APPLICANT: University of Utah Research Foundation
TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides

FILE REFERENCE: Uses of Alpha-Conotoxins
 CURRENT APPLICATION NUMBER: US/09/897,465
 CURRENT FILING DATE: 2001-07-03
 PRIOR APPLICATION NUMBER: US 60/080,588
 PRIOR FILING DATE: 1998-04-03
 PRIOR APPLICATION NUMBER: US 60/070,153
 PRIOR FILING DATE: 1997-12-31
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 8
 LENGTH: 16
 TYPE: PRT
 ORGANISM: Conus aulicus
 -09-897-465-8

Query Match 30.1%; Score 37; DB 9; Length 16;
 Best Local Similarity 33.3%; Pred. No. 2.1e+02;
 Matches 5; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 5 CCLIPACRRNHKKFC 19
 ||||| :
 2 CCGYPPCFATNSGYC 16

SULT 28
 -10-196-394-34
 Sequence 34, Application US/10196394
 Publication No. US20030171278A1
 GENERAL INFORMATION:
 APPLICANT: Mark S. Dennis
 TITLE OF INVENTION: Compounds that Bind HER2
 FILE REFERENCE: P1713R1
 CURRENT APPLICATION NUMBER: US/10/196,394
 CURRENT FILING DATE: 2002-07-15
 PRIOR APPLICATION NUMBER: US/09/609,721
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 60/142,232
 PRIOR FILING DATE: 1998-07-02
 NUMBER OF SEQ ID NOS: 162
 SEQ ID NO 34
 LENGTH: 16
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: synthetic peptide sequence
 -10-196-394-34

Query Match 30.1%; Score 37; DB 14; Length 16;
 Best Local Similarity 50.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 1; Mismatches 4; Indels 2; Gaps 1;
 1 FNWR--CCLIPACR 12
 ||||| :
 1 FNWEKNGCIGPCR 14

SULT 29
 -10-072-602B-609
 Sequence 609, Application US/10072602B
 Publication No. US20030109670A1
 GENERAL INFORMATION:
 APPLICANT: University of Utah Research Foundation
 APPLICANT: Cognetix, Inc.
 APPLICANT: Olivera, Baldomero M.
 APPLICANT: McIntosh, J. Michael
 APPLICANT: Watkins, Maren
 APPLICANT: Garrett, James E.
 APPLICANT: Cruz, Lourdes J.
 APPLICANT: Grilley, Michelle
 APPLICANT: Schoenfeld, Robert M.
 APPLICANT: Walker, Craig
 APPLICANT: Shetty, Reshma
 APPLICANT: Jones, Robert M.

FILE REFERENCE: Cone Snail Peptides
 FILE REFERENCE: 2314-249
 CURRENT APPLICATION NUMBER: US/10/072,602B
 CURRENT FILING DATE: 2002-02-11
 PRIOR APPLICATION NUMBER: US 60/267,408
 PRIOR FILING DATE: 2001-02-09
 NUMBER OF SEQ ID NOS: 638
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 609
 LENGTH: 17
 TYPE: PRT
 ORGANISM: Conus nobilis
 US-10-072-602B-609

Query Match 30.1%; Score 37; DB 14; Length 17;
 Best Local Similarity 40.0%; Pred. No. 2.2e+02;
 Matches 6; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19
 ||||| :
 DB 2 CCERPPCRWQNPDLG 16

RESULT 30
 US-09-954-385-346
 Sequence 346, Application US/09954385
 Publication No. US20030100467A1
 GENERAL INFORMATION:
 APPLICANT: Aehle, Wolfgang
 APPLICANT: Baldwin, Toby L.
 APPLICANT: Van Gastel, Franciscus J.C.
 APPLICANT: Janssen, Giselle G.
 APPLICANT: Murray, Christopher J.
 APPLICANT: Wang, Huaming
 APPLICANT: Winetzkzy, Deborah S.
 TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
 FILE REFERENCE: GC690
 CURRENT APPLICATION NUMBER: US/09/954,385
 CURRENT FILING DATE: 2001-09-12
 NUMBER OF SEQ ID NOS: 433
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 346
 LENGTH: 12
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: binding peptide
 US-09-954-385-346

Query Match 29.3%; Score 36; DB 10; Length 12;
 Best Local Similarity 83.3%; Pred. No. 2.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 RCCLIP 9
 ||||| :
 DB 7 RCCLLP 12

RESULT 31
 US-09-910-009A-170
 Sequence 170, Application US/09910009A
 Publication No. US20030050234A1
 GENERAL INFORMATION:
 APPLICANT: University of Utah Research Foundation
 APPLICANT: Cognetix, Inc.
 APPLICANT: Olivera, Baldomero M.
 APPLICANT: McIntosh, J. Michael
 APPLICANT: Garrett, James E.
 APPLICANT: Watkins, Maren
 APPLICANT: Cruz, Lourdes J.
 APPLICANT: Shon, Ki-Joon
 APPLICANT: Jacobsen, Richard

```
APPLICANT: Jones, Robert M.
APPLICANT: Cartier, G. Edward
APPLICANT: Shen, Greg S.
APPLICANT: Wagstaff, John D.
TITLE OF INVENTION: Mu-Conopeptides
FILE REFERENCE: 2314-242
CURRENT FILING DATE: 2001-07-23
PRIORITY APPLICATION NUMBER: US 60/219,619
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/245,157
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/264,319
PRIOR FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: US 60/277,270
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 520
SOFTWARE: PatentIn version 3.0
SEQ ID NO 170
LENGTH: 16
TYPE: PRT
ORGANISM: Conus marmoreus
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(16)
OTHER INFORMATION: Xaa at residue 4 and 13 is Pro or Hyp
-09-910-009A-170
Query Match 29.3%; Score 36; DB 10; Length 16;
Best Local Similarity 40.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
5 CCLIPACRNHHKFC 19
1 CCAXSACRLGCRXC 15
SULT 32
-09-910-009A-171
Sequence 171, Application US/09910009A
Publication No. US20030050234A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Garrett, James E.
APPLICANT: Watkins, Maren
APPLICANT: Cruz, Lourdes J.
APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
APPLICANT: Cartier, G. Edward
APPLICANT: Shen, Greg S.
APPLICANT: Wagstaff, John D.
TITLE OF INVENTION: Mu-Conopeptides
FILE REFERENCE: 2314-242
CURRENT FILING DATE: 2001-07-23
PRIORITY APPLICATION NUMBER: US 60/219,619
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/245,157
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/264,319
PRIOR FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: US 60/277,270
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 520
SOFTWARE: PatentIn version 3.0
SEQ ID NO 171
LENGTH: 16
TYPE: PRT
ORGANISM: Conus marmoreus
```

```
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(16)
OTHER INFORMATION: Xaa at residue 4 and 13 is Pro or Hyp
US-09-910-009A-171
Query Match 29.3%; Score 36; DB 10; Length 16;
Best Local Similarity 40.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
5 CCLIPACRNHHKFC 19
1 CCAXSACRLGCRXC 15
RESULT 33
US-09-910-009A-172
Sequence 172, Application US/09910009A
Publication No. US20030050234A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Garrett, James E.
APPLICANT: Watkins, Maren
APPLICANT: Cruz, Lourdes J.
APPLICANT: Shon, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
APPLICANT: Cartier, G. Edward
APPLICANT: Shen, Greg S.
APPLICANT: Wagstaff, John D.
TITLE OF INVENTION: Mu-Conopeptides
FILE REFERENCE: 2314-242
CURRENT FILING DATE: 2001-07-23
PRIORITY APPLICATION NUMBER: US 60/219,619
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/245,157
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/264,319
PRIOR FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: US 60/277,270
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 520
SOFTWARE: PatentIn version 3.0
SEQ ID NO 172
LENGTH: 16
TYPE: PRT
ORGANISM: Conus marmoreus
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(16)
OTHER INFORMATION: Xaa at residue 4 and 13 is Pro or Hyp
US-09-910-009A-172
Query Match 29.3%; Score 36; DB 10; Length 16;
Best Local Similarity 40.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
5 CCLIPACRNHHKFC 19
1 CCAXSACRLGCRXC 15
RESULT 34
US-09-910-009A-442
Sequence 442, Application US/09910009A
Publication No. US20030050234A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
```

APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Garrett, James E.
APPLICANT: Watkins, Maren
APPLICANT: Cruz, Lourdes J.
APPLICANT: Shon, Ki-Oon
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
APPLICANT: Cartier, G. Edward
APPLICANT: Shen, Greg S.
APPLICANT: Wagstaff, John D.
TITLE OF INVENTION: Mu-Conopeptides
FILE REFERENCE: 2314-242
CURRENT APPLICATION NUMBER: US/09/910,009A
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,619
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/245,157
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/264,319
PRIOR FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: US 60/277,270
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 520
SOFTWARE: PatentIn version 3.0
SEQ ID NO 442
LENGTH: 16
TYPE: PRT
ORGANISM: Conus marmoreus
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(16)
OTHER INFORMATION: Xaa is Hyp
-09-910-009A-442

Query Match 29.3%; Score 36; DB 10; Length 16;
Best Local Similarity 40.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

5 CCLIPACGRNHKKFC 19
||| |||
1 CCAXSACRLGCRXC 15

SULT 35
-10-072-602B-429
Sequence 429, Application US/10072602B
Publication No. US20030109670A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Watkins, Maren
APPLICANT: Garrett, James E.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Grilley, Michelle
APPLICANT: Schoenfeld, Robert M.
APPLICANT: Walker, Craig
APPLICANT: Shetty, Reshma
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Cone Snail Peptides
FILE REFERENCE: 2314-249
CURRENT APPLICATION NUMBER: US/10/072,602B
CURRENT FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/267,408
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 638
SOFTWARE: PatentIn version 3.0
SEQ ID NO 429
LENGTH: 16
TYPE: PRT
ORGANISM: Conus leopardus

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(16)
OTHER INFORMATION: Xaa at residues 5 and 12 is Pro or hydroxy-Pro; Xaa at residue 1 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
US-10-072-602B-429

Query Match 29.3%; Score 36; DB 14; Length 16;
Best Local Similarity 40.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 5 CCLIPACGRNHKKFC 19
DB 1 CCNXACNRXNKAIC 15

Search completed: February 18, 2004, 06:34:10
Job time : 35 secs

APPLICANT: Luo, Sigin
APPLICANT: University of Utah Research Foundation
TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
FILE REFERENCE: Uses of Alpha-Conotoxins
CURRENT APPLICATION NUMBER: US/09/219,446B
CURRENT FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 60/080,588
PRIOR FILING DATE: 1998-04-03
PRIOR APPLICATION NUMBER: US 60/070,153
PRIOR FILING DATE: 1997-12-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 10
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: A10L derivative
OTHER INFORMATION: of C. purpurascens Fh1A
-09-219-446B-10

Query Match 38.2%; Score 47; DB 3; Length 16;
Best Local Similarity 40.0%; Pred. No. 5-2;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
5 CCLIPACRRNHKKFC 19
|||:|:|:|:
2 CCLPPCALNPDYC 16

RESULT 3
Sequence 32, Application US/08137800
Patent No. 5514774
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: McIntosh, J. Michael
APPLICANT: Santos, Ameurfin S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1000
CITY: Washington
STATE: DC
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,800
FILING DATE: 19-OCT-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-104763
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:

ORGANISM: Conus ermineus
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3..4
OTHER INFORMATION: /note= "Xaa is Pro or Hydroxy-Pro"
US-08-137-800-32
Query Match 37.4%; Score 46; DB 1; Length 18;
Best Local Similarity 46.7%; Pred. No. 7.7;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
5 CCLIPACRRNHKKFC 19
|||:|:|:|:
4 CCSNPACNVNPPQIC 18

RESULT 4
US-08-477-383-32
Sequence 32, Application US/08477383
Patent No. 5589340
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurfin S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,383
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Conus ermineus
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /note= "Xaa is Pro or Hydroxy-Pro."
FEATURE:
NAME/KEY: Modified-site

LOCATION: 18
OTHER INFORMATION: /note= "The C-terminus is
OTHER INFORMATION: preferably amidated."
08-477-383-32

Query Match 37.4%; Score 46; DB 1; Length 18;
Best Local Similarity 46.7%; Pred. No. 7.7;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19
||| : :
Db 4 CCSNPACVNVNPQIC 18

RESULT 6
US-08-480-750-32
; Sequence 32, Application US/08480750
; Patent No. 5633347
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Hillyard, David R.
; APPLICANT: Macintosh, J. Michael
; APPLICANT: Santos, Ameurfino S.
; TITLE OF INVENTION: Conotoxin Peptides
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,750
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/137,800
; FILING DATE: 19-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/084,848
; FILING DATE: 29-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24260-107673
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Conus ermineus
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /note= "Xaa is Pro or Hydroxy-Pro."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 18
; OTHER INFORMATION: /note= "The C-terminus is
; OTHER INFORMATION: preferably amidated."
; US-08-480-750-32

Query Match 37.4%; Score 46; DB 1; Length 18;
Best Local Similarity 46.7%; Pred. No. 7.7;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKFC 19
||| | : :
4 CCSNPACVNVNPQIC 18

SULT 7

-08-477-383-54
Sequence 54, Application US/08477383
Patent No. 5589340
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurfino S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,383
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993

ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear

MOLECULE TYPE: peptide
HYPOTHETICAL: NO

ORIGINAL SOURCE:
ORGANISM: Conus magus

FEATURE:
NAME/KEY: Modified-site

LOCATION: 16
OTHER INFORMATION: /note= "The C-terminus is

amidated."

-08-477-383-54

Query Match 35.8%; Score 44; DB 1; Length 16;
Best Local Similarity 40.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

5 CCLIPACRRNHKFC 19

Db 2 CCSNPVCHLEHSLC 16

RESULT 8

US-08-487-174-54
Sequence 54, Application US/08487174
Patent No. 5595972
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurfino S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,174

FILING DATE: 07-JUN-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993

ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673

TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear

MOLECULE TYPE: peptide
HYPOTHETICAL: NO

ORIGINAL SOURCE:
ORGANISM: Conus magus

FEATURE:
NAME/KEY: Modified-site

LOCATION: 16
OTHER INFORMATION: /note= "The C-terminus is

amidated."

US-08-487-174-54
Query Match 35.8%; Score 44; DB 1; Length 16;
Best Local Similarity 40.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKFC 19

Db 2 CCSNPVCHLEHSLC 16

RESULT 9

US-08-480-750-54

Sequence 54, Application US/08480750
Patent No. 5633347

GENERAL INFORMATION:

APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hilliard, David R.
APPLICANT: McIntosh, J. Michael
APPLICANT: Santos, Aneurfino S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/480,750
FILING DATE: 07-JUN-1995

CLASSIFICATION:

530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/137,800

FILING DATE: 19-OCT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/084,848

FILING DATE: 29-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 24260-107673

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-962-4810

TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 54:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Conus magus

FEATURE:

NAME/KEY: Modified-site

LOCATION: 16

OTHER INFORMATION:

/note= "The C-terminus is

amidated."

-08-480-750-54

Query Match 35.8%; Score 44; DB 1; Length 16;

Best Local Similarity 40.0%; Pred. No. 13;

Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19

DB 2 CCSNPVCHLEHSLC 16

SUJT 10

-09-219-446B-2

Sequence 2, Application US/09219446B

Patent No. 6265541

GENERAL INFORMATION:

APPLICANT: Olivera, Baldomero M.

APPLICANT: McIntosh, J. Michael

APPLICANT: Yoshikami, Doju

APPLICANT: Cartier, G. Edward

APPLICANT: Luo, Siqin

APPLICANT: University of Utah Research Foundation

TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides

FILE REFERENCE: Uses of Alpha-Conotoxins

CURRENT APPLICATION NUMBER: US/09/219,446B

CURRENT FILING DATE: 1998-12-23

PRIOR APPLICATION NUMBER: US 60/080,588

PRIOR FILING DATE: 1998-04-03

PRIOR APPLICATION NUMBER: US 60/070,153

PRIOR FILING DATE: 1997-12-31

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 16

TYPE: PRT

ORGANISM: Conus magus

US-09-219-446B-2

Query Match 35.8%; Score 44; DB 3; Length 16;

Best Local Similarity 40.0%; Pred. No. 13;

Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19

DB 2 CCSNPVCHLEHSLC 16

RESULT 11

US-09-219-446B-3

Sequence 3, Application US/09219446B

Patent No. 6265541

GENERAL INFORMATION:

APPLICANT: Olivera, Baldomero M.

APPLICANT: McIntosh, J. Michael

APPLICANT: Yoshikami, Doju

APPLICANT: Cartier, G. Edward

APPLICANT: Luo, Siqin

APPLICANT: University of Utah Research Foundation

TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides

FILE REFERENCE: Uses of Alpha-Conotoxins

CURRENT APPLICATION NUMBER: US/09/219,446B

CURRENT FILING DATE: 1998-12-23

PRIOR APPLICATION NUMBER: US 60/080,588

PRIOR FILING DATE: 1998-04-03

PRIOR APPLICATION NUMBER: US 60/070,153

PRIOR FILING DATE: 1997-12-31

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3

LENGTH: 17

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Tyr derivative

OTHER INFORMATION: of C. magus MII

US-09-219-446B-3

Query Match 35.8%; Score 44; DB 3; Length 17;

Best Local Similarity 40.0%; Pred. No. 13;

Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19

DB 3 CCSNPVCHLEHSLC 17

RESULT 12

US-08-084-848A-8

Sequence 8, Application US/08084848A

Patent No. 5432155

GENERAL INFORMATION:

APPLICANT: Olivera, Baldomero M.

APPLICANT: Rivier, Jean E. F.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Abogadie, Fe
APPLICANT: Hopkins, Chris E.
APPLICANT: Dykert, John
APPLICANT: Torres, Josep L.
TITLE OF INVENTION: Conotoxins I
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitch, Even, Tabin & Flannery
STREET: 135 South LaSalle Street, Suite 900
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/084,848A
FILING DATE: June 29, 1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Schumann, James J.
REGISTRATION NUMBER: 20856
REFERENCE/DOCKET NUMBER: 52511
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)552-1311
TELEFAX: (619)552-0095
TELEX: 20 6566 PATLAW CGO
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
-08-084-848A-8
Query Match 35.8%; Score 44; DB 1; Length 19;
Best Local Similarity 40.0%; Pred. No. 15;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
5 CCLIPACRRNHKKFC 19
2 CCSHPACSGKYQYXC 16
RESULT 13
-08-458-499-8
Sequence 8, Application US/08458499
Patent No. 5700778
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Rivier, Jean E. F.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Abogadie, Fe
APPLICANT: Hopkins, Chris E.
APPLICANT: Dykert, John
APPLICANT: Torres, Josep L.
TITLE OF INVENTION: Conotoxins I
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitch, Even, Tabin & Flannery
STREET: 135 South LaSalle Street, Suite 900
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,499
FILING DATE: 02-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/084,848
FILING DATE: June 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Schumann, James J.
REGISTRATION NUMBER: 20856
REFERENCE/DOCKET NUMBER: 52511
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)552-1311
TELEFAX: (619)552-0095
TELEX: 20 6566 PATLAW CGO
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-458-499-8
Query Match 35.8%; Score 44; DB 1; Length 19;
Best Local Similarity 40.0%; Pred. No. 15;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
5 CCLIPACRRNHKKFC 19
2 CCSHPACSGKYQYXC 16
Db
RESULT 14
US-09-219-446B-11
Sequence 11, Application US/09219446B
Patent No. 6265541
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: McIntosh, J. Michael
APPLICANT: Yoshikami, Doju
APPLICANT: Cartier, G. Edward
APPLICANT: Luo, Sigin
APPLICANT: University of Utah Research Foundation
TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
FILE REFERENCE: Uses of Alpha-Conotoxins
CURRENT APPLICATION NUMBER: US/09/219,446B
CURRENT FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 60/080,588
PRIOR FILING DATE: 1998-04-03
PRIOR APPLICATION NUMBER: US 60/070,153
PRIOR FILING DATE: 1997-12-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: N11S derivative
of C. purpurascens Pn1A
US-09-219-446B-11
Query Match 35.0%; Score 43; DB 3; Length 16;
Best Local Similarity 33.3%; Pred. No. 17;
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
5 CCLIPACRRNHKKFC 19
2 CCSLPFCAASNPDC 16
Db

```
ULT 15
09-136-769A-3
sequence 3, Application US/09136769A
Patent No. 6307014
GENERAL INFORMATION:
APPLICANT: Furie, Bruce
APPLICANT: Furie, Barbara
APPLICANT: Stenflo, Johan
APPLICANT: Rigby, Alan C.
APPLICANT: Roepstoft, Peter
TITLE OF INVENTION: CONOPEPTIDES
FILE REFERENCE: 50065/002001
CURRENT APPLICATION NUMBER: US/09/136.769A
CURRENT FILING DATE: 1998-08-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 19
TYPE: PRT
ORGANISM: Conus textile
FEATURE:
NAME/KEY: VARIANT
LOCATION: (2)...(16)
OTHER INFORMATION: Pro at position 2 is 4Hyp and each Xaa is
OTHER INFORMATION: Independently selected from Glu and
OTHER INFORMATION: gamma-carboxyglutamic acid, provided that at least
OTHER INFORMATION: one Xaa is gamma-carboxyglutamic acid.
NAME/KEY: VARIANT
LOCATION: (1)...(19)
OTHER INFORMATION: Xaa = Any Amino Acid
NAME/KEY: VARIANT
LOCATION: (1)...(19)
OTHER INFORMATION: Xaa = Any Amino Acid
09-136-769A-3

Query Match 35.0%; Score 43; DB 4; Length 19;
Best Local Similarity 40.0%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19
Db 4 CCSDPRCNSHPXLC 18

RESULT 17
US-09-219-446B-4
; Sequence 4, Application US/09219446B
; Patent No. 6265541
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Yoshikami, Doju
; APPLICANT: Cartier, G. Edward
; APPLICANT: Luo, Siglin
; APPLICANT: University of Utah Research Foundation
; TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
; FILE REFERENCE: Uses of Alpha-Conotoxins
; CURRENT APPLICATION NUMBER: US/09/219,446B
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/080,588
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: US 60/070,153
; PRIOR FILING DATE: 1997-12-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: FAT derivative
; OTHER INFORMATION: of C. magus MII
US-09-219-446B-4

Query Match 34.1%; Score 42; DB 3; Length 16;
Best Local Similarity 40.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKKFC 19
Db 2 CCNPFVCFATHSNLC 16

RESULT 18
US-09-219-446B-12
; Sequence 12, Application US/09219446B
; Patent No. 6265541
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Yoshikami, Doju
; APPLICANT: Cartier, G. Edward
; APPLICANT: Luo, Siglin
; APPLICANT: University of Utah Research Foundation
; TITLE OF INVENTION: Uses of Alpha-Conotoxin Peptides
; FILE REFERENCE: Uses of Alpha-Conotoxins
; CURRENT APPLICATION NUMBER: US/09/219,446B
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/080,588
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: US 60/070,153
; PRIOR FILING DATE: 1997-12-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
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SEQ ID NO 12
LENGTH: 16

TYPE: PRT
ORGANISM: Conus purpurascens
-09-219-446B-12

Query Match 34.1%; Score 42; DB 3; Length 16;
Best Local Similarity 33.3%; Pred. No. 23;
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

5 CCLIPACRRNHKFC 19
||:|:|:|:
2 CGLPFCALSNPDYC 16

SULT 19

US-08-137-800-17
Sequence 17, Application US/08137800
Patent No. 5514774

GENERAL INFORMATION:

APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: McIntosh, J. Michael
APPLICANT: Santos, Ameurfin S.

TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1000
CITY: Washington
STATE: DC

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/137,800
FILING DATE: 19-OCT-1993
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-104763

TELEPHONE: 202-962-4810

TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Conus characteristicus

FEATURE:

NAME/KEY: Modified-site

LOCATION: 15..16

OTHER INFORMATION: /note= "Xaa is Ser or Asn"

-08-137-800-17

Query Match 33.3%; Score 41; DB 1; Length 16;
Best Local Similarity 50.0%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

5 CCLIPACRRNHK 16

||:|:|:|:
3 CCSIPSCWEKYK 14

RESULT 20

US-08-477-383-17

Sequence 17, Application US/08477383
Patent No. 5589340

GENERAL INFORMATION:

APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael

APPLICANT: Santos, Ameurfin S.

TITLE OF INVENTION: Conotoxin Peptides

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,383

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/137,800

FILING DATE: 19-OCT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/084,848

FILING DATE: 29-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 24260-107673

TELEPHONE: 202-962-4810

TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Conus characteristicus

FEATURE:

NAME/KEY: Modified-site

LOCATION: 16

OTHER INFORMATION: /note= "Xaa is Ser or Asn."

US-08-477-383-17

Query Match 33.3%; Score 41; DB 1; Length 16;

Best Local Similarity 50.0%; Pred. No. 30;

Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY

5 CCLIPACRRNHK 16

||:|:|:|:
3 CCSIPSCWEKYK 14

Db

RESULT 21

US-08-487-174-17

Sequence 17, Application US/08487174

Patent No. 5595972

GENERAL INFORMATION:

APPLICANT: Olivera, Baldomero M.

APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurfin S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0; Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,174
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Conus characteristic
FEATURE:
NAME/KEY: Modified-site
LOCATION: 16
OTHER INFORMATION: /note= "Xaa is Ser or Asn."
-08-487-174-17

Query Match 33.3%; Score 41; DB 1; Length 16;
Best Local Similarity 50.0%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

5 CCLIPACRRNHK 16
3 CCSIPSCWEYK 14

RESULT 22
-08-480-750-17
Sequence 17, Application US/08480750
Patent No. 563347
GENERAL INFORMATION:
APPLICANT: Olivera, Balomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurfin S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0; Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,750
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Conus characteristic
FEATURE:
NAME/KEY: Modified-site
LOCATION: 16
OTHER INFORMATION: /note= "Xaa is Ser or Asn."
US-08-480-750-17

Query Match 33.3%; Score 41; DB 1; Length 16;
Best Local Similarity 50.0%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

5 CCLIPACRRNHK 16
3 CCSIPSCWEYK 14

RESULT 23
US-08-116-733-7
Sequence 7, Application US/08116733
Patent No. 551632
GENERAL INFORMATION:
APPLICANT: PALKER, Thomas J.
APPLICANT: HAYNES, Barton F.
TITLE OF INVENTION: SYNTHETIC PEPTIDES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHUYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,733
FILING DATE: 07-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-33
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200787 NIXN UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
-08-116-733-7

Query Match 32.5%; Score 40; DB 1; Length 14;
Best Local Similarity 54.5%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

1 FNRRCCLIPAC 11
|||||
4 FNTWTCFDPQC 14

SULT 24

-08-469-615-5
Sequence 5, Application US/08469615
Patent No. 5622703

GENERAL INFORMATION:
APPLICANT: Berzofsky, Jay A.
APPLICANT: Kurata, Akihiko
TITLE OF INVENTION: Immunodominant Sites of HTLV-I Envelope
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,615
FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/243,118

FILING DATE: 16-MAY-1994

ATTORNEY/AGENT INFORMATION:

NAME: Svensson, Leonard R.

REGISTRATION NUMBER: 30330

REFERENCE/DOCKET NUMBER: 1173-500P

TELEPHONE: 703-205-8000

TELEFAX: 703-205-8050

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: peptide

HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE: HTLV-I
ORGANISM: HTLV-I
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..14
OTHER INFORMATION: /label= peptide_sps
US-08-469-615-5

Query Match 32.5%; Score 40; DB 1; Length 14;
Best Local Similarity 54.5%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 FNRRCCLIPAC 11
|||||
Db 4 FNTWTCFDPQC 14

RESULT 25

US-08-466-763-5
Sequence 5, Application US/08466763
Patent No. 5695762

GENERAL INFORMATION:
APPLICANT: Berzofsky, Jay A.
APPLICANT: Kurata, Akihiko
TITLE OF INVENTION: Immunodominant Sites of HTLV-I Envelope
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,763
FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/243,118

FILING DATE: 16-MAY-1994

ATTORNEY/AGENT INFORMATION:

NAME: Svensson, Leonard R.

REGISTRATION NUMBER: 30330

REFERENCE/DOCKET NUMBER: 1173-497P

TELEPHONE: 703-205-8000

TELEFAX: 703-205-8050

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

FRAGMENT TYPE: internal

ORIGINAL SOURCE:

ORGANISM: HTLV-I

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..14

OTHER INFORMATION: /label= peptide_sps

US-08-466-763-5

Query Match 32.5%; Score 40; DB 1; Length 14;

Best Local Similarity 54.5%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

1 FNRRCCLIPAC 11
||| |
4 FNRWCFDPQC 14

SULT 26

-08-411-142A-5
Sequence 5, Application US/08411142A
Patent No. 5882853

GENERAL INFORMATION:

APPLICANT: Berzofsky, Jay A.

APPLICANT: Kurata, Akihiko

TITLE OF INVENTION: METHOD OF EVALUATING HTLV-I-SPECIFIC

TITLE OF INVENTION: T CELL RESPONSES

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA

COUNTRY: US

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/411,142A

FILING DATE: 27-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/243,118

FILING DATE: 16-MAY-1994

APPLICATION NUMBER: 07/401,411

FILING DATE: 01-SEP-1989

ATTORNEY/AGENT INFORMATION:

NAME: Wetherell, Jr., Ph.D, John R.

REGISTRATION NUMBER: 31,678

REFERENCE/DOCKET NUMBER: 08830/026002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

IMMEDIATE SOURCE:

CLONE: HTLV-I

-08-411-142A-5

Query Match 32.5%; Score 40; DB 2; Length 14;

Best Local Similarity 54.5%; Pred. No. 37;

Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

1 FNRRCCLIPAC 11

||| |

4 FNRWCFDPQC 14

SULT 27

-08-137-800-15

Sequence 15, Application US/08137800

Patent No. 5514774

GENERAL INFORMATION:

APPLICANT: Olivera, Baldomero M.

APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: McIntosh, J. Michael
APPLICANT: Santos, Ameurfin D.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1000
CITY: Washington
STATE: DC
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/137,800

FILING DATE: 19-OCT-1993

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 24260-104763

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-962-4810

TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORGANISM: Conus bandanus

FEATURE:

NAME/KEY: Modified-site

LOCATION: 6..13

OTHER INFORMATION: /note= "Xaa(6) is Pro or

OTHER INFORMATION: Hydroxy-Pro; Xaa(13) is Pro or Hydroxy-Pro"

US-08-137-800-15

Query Match 32.5%; Score 40; DB 1; Length 16;

Best Local Similarity 40.0%; Pred. No. 41;

Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 5 CCLIPACRRNHKFC 19

||| |

Db 2 COTHXACHVSHXELC 16

RESULT 28

US-08-477-383-15

Sequence 15, Application US/08477383

Patent No. 5589340

GENERAL INFORMATION:

APPLICANT: Olivera, Baldomero M.

APPLICANT: Cruz, Lourdes J.

APPLICANT: Hillyard, David R.

APPLICANT: McIntosh, J. Michael

APPLICANT: Santos, Ameurfin S.

TITLE OF INVENTION: Conotoxin Peptides

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti

STREET: 1201 New York Avenue, N.W., Suite 1000

CITY: Washington

STATE: DC

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,383
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Conus bandanus
FEATURE:
NAME/KEY: Modified-site
LOCATION: 16
OTHER INFORMATION: /note= "The C-terminus is
OTHER INFORMATION: preferably amidated."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6..13
OTHER INFORMATION: /note= "Xaa(6) is Pro or
OTHER INFORMATION: Hydroxy-Pro; Xaa(13) is Pro or Hydroxy-Pro."
US-08-477-383-15
Query Match 32.58; Score 40; DB 1; Length 16;
Best Local Similarity 40.0%; Pred. No. 41;
Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19
||| : : :
2 CCTXACHVSHXELC 16

RESULT 29
US-08-487-174-15
Sequence 15, Application US/08487174
Patent No. 5595972
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurfino S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,174
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Conus bandanus
FEATURE:
NAME/KEY: Modified-site
LOCATION: 16
OTHER INFORMATION: /note= "The C-terminus is
OTHER INFORMATION: preferably amidated."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6..13
OTHER INFORMATION: /note= "Xaa(6) is Pro or
OTHER INFORMATION: Hydroxy-Pro; Xaa(13) is Pro or Hydroxy-Pro."
US-08-487-174-15
Query Match 32.5%; Score 40; DB 1; Length 16;
Best Local Similarity 40.0%; Pred. No. 41;
Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19
||| : : :
2 CCTXACHVSHXELC 16

RESULT 30
US-08-480-750-15
Sequence 15, Application US/08480750
Patent No. 5633347
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurfino S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,750
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Conus bandanus
FEATURE:
NAME/KEY: Modified-site
LOCATION: 16
OTHER INFORMATION: /note= "The C-terminus is
OTHER INFORMATION: preferably amidated."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6, 13
OTHER INFORMATION: /note= "Xaa(6) is Pro or
OTHER INFORMATION: Hydroxy-Pro; Xaa(13) is Pro or Hydroxy-Pro."
-08-480-750-15
Query Match 32.5%; Score 40; DB 1; Length 16;
Best Local Similarity 40.0%; Pred. No. 41;
Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
5 CCLIPACRNHHKFC 19
|||:|:|
2 CCTHAXCHVSHXELC 16
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SULT 31
-08-137-800-13
Sequence 13, Application US/08137800
Patent No. 5514774
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: McIntosh, J. Michael
APPLICANT: Santos, Ameurfin D.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1000
CITY: Washington
STATE: DC
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,800
FILING DATE: 19-OCT-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-104763
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Conus ermineus
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3, 4
OTHER INFORMATION: /note= "Xaa is Pro or Hydroxy-Pro"
US-08-137-800-13
Query Match 32.5%; Score 40; DB 1; Length 18;
Best Local Similarity 33.3%; Pred. No. 45;
Matches 5; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 5 CCLIPACRNHHKFC 19
DB 4 CCYHETCNMNPQIC 18
RESULT 32
US-08-137-800-31
Sequence 31, Application US/08137800
Patent No. 5514774
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: McIntosh, J. Michael
APPLICANT: Santos, Ameurfin D.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1000
CITY: Washington
STATE: DC
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,800
FILING DATE: 19-OCT-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-104763
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
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LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Conus ermineus
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3..4
OTHER INFORMATION: /note= "Xaa is Pro or Hydroxy-Pro"
3-08-137-800-31
Query Match 32.5%; Score 40; DB 1; Length 18;
Best Local Similarity 33.3%; Pred. No. 45;
Matches 5; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
/ 5 CCLIPACRRNHKFC 19
4 CCYHPTCNMSNPQC 18
RESULT 33
3-08-477-383-13
Sequence 13, Application US/08477383
Patent No. 5589340
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurfino S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,383
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:

ORGANISM: Conus ermineus
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /note= "Xaa is Pro or Hydroxy-Pro."
US-08-477-383-13
Query Match 32.5%; Score 40; DB 1; Length 18;
Best Local Similarity 33.3%; Pred. No. 45;
Matches 5; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 5 CCLIPACRRNHKFC 19
DB 4 CCYHPTCNMSNPQC 18
RESULT 34
US-08-477-383-31
Sequence 31, Application US/08477383
Patent No. 5589340
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurfino S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,383
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Conus ermineus
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /note= "Xaa is Pro or Hydroxy-Pro."
NAME/KEY: Modified-site

LOCATION: 18
OTHER INFORMATION: /note= "The C-terminus is
OTHER INFORMATION: preferably amidated."
:-08-477-383-31

Query Match 32.5%; Score 40; DB 1; Length 18;
Best Local Similarity 33.3%; Pred. No. 45;
Matches 5; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

5 CCLIPACRRNHKKFC 19
4 CCYHPTCNMSNPQIC 18

RESULT 35

:-08-487-174-13
Sequence 13, Application US/08487174
Patent No. 5595972

GENERAL INFORMATION:

APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Aneurfino S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,174
FILING DATE: 07-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 24260-107673
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO

ORIGINAL SOURCE:
ORGANISM: Conus ermineus
FEATURE:

NAME/KEY: Modified-site
LOCATION: 3

OTHER INFORMATION: /note= "Xaa is Pro or Hydroxy-Pro."

:-08-487-174-13

Query Match

Best Local Similarity 32.5%; Score 40; DB 1; Length 18;

Matches 5; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Matches 5; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 5 CCLIPACRRNHKKFC 19

Db 4 CCYHPTCNMSNPQIC 18

Search completed: February 18, 2004, 06:29:56

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